Polyketides and their synthesis

Field of Invention

The present invention relates to processes and materials (including recombinant strains) for the preparation and isolation of macrolide compounds, particularly compounds differing from natural compounds at least in terms of glycosylation. It is particularly concerned with erythromycin and azithromycin analogues wherein the natural sugar at the 5-position has been replaced. The invention includes the use of recombinant cells in which gene cassettes are expressed to generate novel macrolide antibiotics.

Background to the Invention

The biosynthetic pathways to the macrolide antibiotics produced by actinomycete bacteria generally involve the assembly of an aglycone structure, followed by specific modifications which may include any or all of: hydroxylation or other oxidative steps, methylation and glycosylation. In the case of the 14-membered macrolide erythromycin A, these modifications consist of the specific hydroxylation of 6-deoxyerythronolide B to erythronolide B which is catalysed by EryF, followed by the sequential attachment of dTDP-L mycarose via the hydroxyl group at C-3 catalysed by the mycarosyltransferase EryBV (Staunton and Wilkinson, 1997). The attachment of dTDP-D-desosamine via the hydroxyl group at C-5, catalysed by EryCIII, then results in the production of erythromycin D, the first intermediate with antibiotic activity. Erythromycin D is subsequently converted to erythromycin A by hydroxylation at C-12 (EryK) and *O*-methylation (EryG) on the mycarosyl group, this order being preferred (Staunton and Wilkinson, 1997). The biosynthesis of dTDP-L-mycarose and dTDP-D-desosamine has been studied in detail (Gaisser *et al.*, 1997; Summers *et al.*, 1997; Gaisser *et al.*, 1998; Salah-Bey *et al.*, 1998).

Recently, a 3.1 Å high-resolution X-ray investigation of the interaction of ribosomes with macrolides (Schlünzen *et al.*, 2001, Hansen *et al.*, 2002) has revealed key interactions giving direct insights into ways in which macrolide templates might be adapted, by chemical or biological approaches, for increased ribosomal binding and inhibition and for improved effectiveness against resistant organisms. In particular, previous indications about the importance of the sugar substituent at the C-5 hydroxyl of the macrocycle for ribosomal binding were fully borne out by the structural analysis. This substituent extends towards the peptidyl transferase centre and in the case of 16-membered macrolides, which bear a disaccharide at C-5, reaches further into the peptidyl transferase centre, thus providing a molecular basis for the observation that 16-membered macrolides inhibit ribosomal capacity to form even a single peptide bond (Poulsen *et al.*, 2000). This suggests that erythromycins with alternative substituents at the C-5 positions, for example mycaminosyl and angolosaminyl erythromycins, and in particular mycaminosyl and 4'-*O* substituted mycaminosyl erythromycins, are highly desirable as potential anti-bacterial agents.

Since post-polyketide synthase modifications are often critical for biological activity (Liu and Thorson, 1994; Kaneko *et al.*, 2000), there has been increasing interest in understanding the mechanism and specificity of the enzymes involved to engineer the biosynthesis of diverse novel hybrid macrolides with potentially improved activities. Recent work has demonstrated that the manipulation of sugar biosynthetic genes is a powerful approach to isolate novel macrolide antibiotics. The recently demonstrated relaxed specificity of the glycosyltransferases is crucial for this approach (see Méndez and Salas, 2001 and references therein). In the pathways to erythromycin A and methymycin / neomethymycin, the production of hybrid macrolides has been observed after inactivation of specific genes involved in the biosynthesis of deoxyhexoses (Gaisser *et al.*, 1997; Summers *et al.*, 1997; Gaisser *et al.*, 1998; Salah-Bey *et al.*, 1998; Zhao *et al.*, 1998a; Zhao *et al.*, 1998b) or after the expression of genes from different biosynthetic gene clusters (Zhao *et al.*, 1999). A relaxed specificity towards the sugar substrate has also been reported for glycosyltransferases that have been expressed in heterologous strains, including glycosyltransferases from the pathways to vancomycin (Solenberg *et al.*, 1997), elloramycin (Wohlert *et al.*, 1998), oleandomycin (Doumith *et al.*, 1999; Gaisser *et al.*, 2000), pikromycin (Tang and McDaniel, 2001), epirubicin (Madduri *et al.*, 1998), avermectin (Wohlert *et al.*, 2001) and spinosyn (Gaisser *et al.*, 2002a). Most of the successful alterations so far reported have involved relaxed specificity towards the activated sugar moiety, while as yet only isolated examples are known where a glycosyltransferase targets its deoxysugar to an alternative aglycone substrate (Spagnoli *et al.*, 1983; Trefzer *et al.*, 1999). Both WO 97/23630 and WO 99/05283 describe the production of erythromycins with an altered glycosylation pattern in culture supernatants by deletion of a specific sugar biosynthesis gene. Thus WO 99/05283 describes low but detectable levels of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin D in the culture supernatant of an *eryCIV* knockout strain of *S. erythraea*. It also has been demonstrated that the use of the gene cassette technology described in patent WO01/79520 is a powerful and potentially general approach to isolate novel macrolide antibiotics by expressing combinations of genes in mutant strains of *S. erythraea* (Gaisser *et al.*, 2002b). WO 01/79520 also describes the detection of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A in culture supernatants of the *S. erythraea* strains SGQ2pSGCIII and SGQ2p(mycaminose)CIII, fed with 3-*O*-mycarosyl erythronolide B. However, the low levels of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A make this a less than optimal method for producing this valuable material on large scales and similar problems were encountered synthesizing 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A using chemical methods (Jones *et al.*, 1969). EP 1024145 refers to the isolation of azithromycin analogues carrying a mycaminosyl residue such as 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin and 3''-desmethyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin. However the only examples given in this area are "prophetic examples" and there is no evidence that they could actually be put into practice.

Therefore, the present invention provides the first demonstration of an efficient and highly effective method for making significant quantities of erythromycins and azithromycins which have non-natural sugars at the C-5 position, in particular mycaminose and angolosamine. In a specific aspect the present invention provides for the synthesis of mycaminose and angolosamine using specific combinations of sugar biosynthetic genes in gene cassettes.

Summary of the Invention

The present invention relates to processes, and recombinant strains, for the preparation and isolation of erythromycins and azithromycins, which differ from the corresponding naturally occurring compound in the glycosylation of the C-5 position. In a specific aspect the present invention relates to processes, and recombinant strains, for the preparation and isolation of erythromycins and azithromycins, which incorporate angolosamine or mycaminose at the C-5 position. In particular, the present invention relates to processes and recombinant strains for the preparation and isolation of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl, or angolosaminyl erythromycins and azithromycins, in particular 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycins and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycins, and specifically 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin B, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin C, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin D, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A, and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin. The present invention further relates to novel 5-*O*-dedesosaminyl-5-*O*-mycaminosyl, angolosaminyl erythromycins and azithromycins produced thereby.

Detailed description of the Invention

The present invention relates to processes, and recombinant strains, for the preparation and isolation of erythromycins and azithromycins which differ from the naturally occurring compound in the glycosylation of the C-5 position. These are referred to herein as "compounds of the invention" and unless the context dictates otherwise, such a reference includes a reference to 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycins, 5-*O*-dedesosaminyl-5-*O*-angolosaminyl erythromycins, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycins, and 5-*O*-dedesosaminyl-5-*O*-angolosaminyl azithromycins, specifically 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin C, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin B, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin D, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin, 5-*O*-dedesosaminyl-5-*O*-angolosaminyl erythromycin A, 5-*O*-dedesosaminyl-5-*O*-angolosaminyl erythromycin B, 5-*O*-dedesosaminyl-5-*O*-angolosaminyl erythromycin C, 5-*O*-dedesosaminyl-5-*O*-angolosaminyl erythromycin D, 5-*O*-dedesosaminyl-5-*O*-angolosaminyl azithromycin and analogues thereof which additionally vary in glycosylation at the C3 position (see WO 01/79520) and which may also vary in the aglycone backbones (see

WO 98/01571, EP 1024145, WO 93/13663, WO 98/49315). The invention relates to processes, and recombinant strains, for the preparation and isolation of compounds of the invention. In particular, the present invention provides a process for the production of erythromycins and azithromycins which differ from the naturally occurring compound in the glycosylation of the C-5 position, said process comprising transforming a strain with a gene cassette as described herein and culturing the strain under appropriate conditions for the production of said erythromycin or azithromycin. In a preferred embodiment the strain is an actinomycete, a pseudomonad, a myxobacterium, or an *E. coli*. In an alternative preferred embodiment the host strain is additionally transformed with the *ermE* gene from *S. erythraea*. In a more highly preferred embodiment, the host strain is an actinomycete. In a more highly preferred embodiment the host strain is selected from *S. erythraea*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces albus*, *Streptomyces lividans*, *Streptomyces hygroscopicus sp.*, *Streptomyces hygroscopicus var. ascomyceticus*, *Streptomyces longisporoflavus*, *Saccharopolyspora spinosa*, *Streptomyces tsukubaensis*, *Streptomyces coelicolor*, *Streptomyces fradiae*, *Streptomyces rimosus*, *Streptomyces avermitilis*, *Streptomyces eurythermus*, *Streptomyces venezuelae*, and *Amycolatopsis mediterranei*. In a specific embodiment the host strain is *S. erythraea*. In an alternative specific embodiment the host strain is selected from the SGQ2, Q42/1 or 18A1 strains of *S. erythraea*.

The present invention further relates to novel 5-*O*-dedesosaminyl-5-*O*-angolosaminyl erythromycins and azithromycins produced thereby (Figure 1). The methodology comprises in part the expression of a gene cassette in the *S. erythraea* mutant strain SGQ2 (which carries genomic deletions in *eryA*, *eryCIII*, *eryBV* and *eryCIV* (WO01/79520)), as described in Example 3 and 6 and in *S. erythraea* Q42/1 (BIOT-2166) (Examples 1- 4) and *S. erythraea* 18A1 (BIOT-2634) (Example 6). Detailed descriptions are given in Examples 1 - 11.

The invention relates to a process involving the transformation of an actinomycete strain, including but not limited to strains of *S. erythraea* such as SGQ2, (see WO 01/79520) or Q42/1 or 18A1 (whose preparation is described below) with an expression plasmid containing a combination of genes which are able to direct the biosynthesis of a sugar moiety and direct its subsequent transfer to an aglycone or pseudoaglycone.

In a particular embodiment the present invention relates to a gene cassette containing a combination of genes which are able to direct the synthesis of mycaminose or angolosamine in an appropriate strain background.

In a particular embodiment the present invention relates to a gene cassette containing a combination of genes which are able to direct the synthesis of mycaminose in an appropriate strain background. The gene cassette may include genes selected from but not limited to *angorf14, tylMIII, tylMI, tylB, tylAI, tylAII, tylIa, angAI, angAII, angMIII, angB, angMI, eryG, eryK* and glycosyltransferase genes including but not limited to *tylMII, angMII, desVII, eryCIII, eryBV, spnP, and midI*. In a preferred

embodiment the gene cassette comprises *tylIa* in combination with one or more other genes which are able to direct the synthesis of mycaminose. In a preferred embodiment the gene cassette comprises *angorf14* in combination with one or more other genes which are able to direct the synthesis of mycaminose. In an more preferred embodiment the gene cassette comprises *angAI, angAII, angorf14, angMIII, angB, angMI,* in combination with one or more glycosyltransferases such as but not limited to *eryCIII, tylMII, angMII,* In an alternative embodiment the gene cassette comprises *tylAI, tylAII, tylMIII, tylB, tylIa, tylMI* in combination with glycosyltransferases such as but not limited to *eryCIII, tylMII* and *angMII.* In a preferred embodiment the strain is an *S. erythraea* strain.

In a particular embodiment the present invention relates to a gene cassette containing combinations of genes which are able to direct the synthesis of angolosamine, including but not limited to *angMIII, angMI, angB, angAI, angAII, angorf14, angorf4, tylMIII, tylMI, tylB, tylAI, tylAII, eryCVI, spnO, eryBVI,* and *eryK* and one or more glycosyltransferase genes including but not limited to *eryCIII, tylMII, angMII, desVII, eryBV, spnP and midI.* In a preferred embodiment the gene cassette contains *angMIII, angMI, angB, angAI, angAII, angorf14, spnO* in combination with a glycosyltransferase gene such as but not limited to *angMII, tylMII* or *eryCIII.* In an alternative preferred embodiment the gene cassette contains comprises *angMIII, angMI, angB, angAI, angAII, angorf4, and angorf14,* in combination with one or more glycosyltransferases selected from the group consisting of *angMII, tylMII* and *eryCIII.* In a preferred embodiment the strain is an *S. erythraea* strain.

In one embodiment, the process of the present invention further involves feeding of an aglycone and/or a pseudoaglycone substrate (for definition see below), to the recombinant strain, said aglycone or pseudoaglycone is selected from the group including (but not limited to) 3-*O*-mycarosyl erythronolide B, erythronolide B, 6-deoxy erythronolide B, 3-*O*-mycarosyl-6-deoxy erythronolide B, tylactone, spinosyn pseudoaglycones, 3-*O*-rhamnosyl erythronolide B, 3-*O*-rhamnosyl-6-deoxy erythronolide B, 3-O-angolosaminyl erythronolide B, 15-hydroxy-3-*O*-mycarosyl erythronolide B, 15-hydroxy erythronolide B, 15-hydroxy-6-deoxy erythronolide B, 15-hydroxy-3-*O*-mycarosyl-6-deoxy erythronolide B, 15-hydroxy-3-*O*-rhamnosyl erythronolide B, 15-hydroxy-3-*O*-rhamnosyl-6-deoxy erythronolide B, 15-hydroxy-3-O-angolosaminyl erythronolide B, 14-hydroxy-3-*O*-mycarosyl erythronolide B, 14-hydroxy erythronolide B, 14-hydroxy-6-deoxy erythronolide B, 14-hydroxy-3-*O*-mycarosyl-6-deoxy erythronolide B, 14-hydroxy-3-*O*-rhamnosyl erythronolide B, 14-hydroxy-3-*O*-rhamnosyl-6-deoxy erythronolide B, 14-hydroxy-3-O-angolosaminyl erythronolide B to cultures of the transformed actinomycete strains, the bioconversion of the substrate to compounds of the invention and optionally the isolation of said compounds. This process is exemplified in Examples 1-11. However, a person of skill in the art will appreciate that in an alternative embodiment the host cell can express the desired aglycone template, either naturally or recombinantly.

As used herein, the term "pseudoaglycone" refers to a partially glycosylated intermediate of a multiply-glycosylated product.

Those skilled in the art will appreciate that alternative host strains can be used. A preferred cell is a prokaryote or a fungal cell or a mammalian cell. A particularly preferred host cell is a prokaryote, more preferably host cell strains such as actinomycetes, *Pseudomonas*, myxobacteria, and *E. coli*. It will be appreciated that if the host cell does not naturally produce erythromycin, or a closely related 14-membered macrolide, it may be necessary to introduce a gene conferring self-resistance to the macrolide product, such as the *ermE* gene from *S. erythraea*. Even more preferably the host cell is an actinomycete, even more preferably strains that include but are not limited to *S. erythraea*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces albus*, *Streptomyces lividans*, *Streptomyces hygroscopicus sp.*, *Streptomyces hygroscopicus var. ascomyceticus*, *Streptomyces longisporoflavus*, *Saccharopolyspora spinosa*, *Streptomyces tsukubaensis*, *Streptomyces coelicolor*, *Streptomyces fradiae*, *Streptomyces rimosus*, *Streptomyces avermitilis*, *Streptomyces eurythermus*, *Streptomyces venezuelae*, *Amycolatopsis mediterranei*. In a more highly preferred embodiment the host cell is *S. erythraea*.

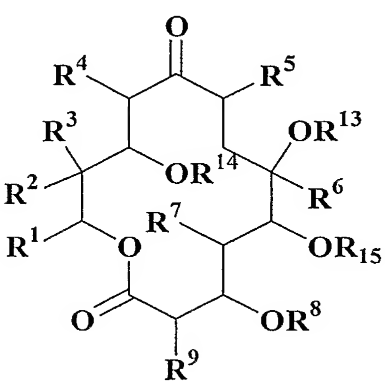
It will readily occur to those skilled in the art that the substrate fed to the recombinant cultures of the invention need not be a natural intermediate in erythromycin biosynthesis. Thus, the substrate could be modified in the aglycone backbone (see Examples 8-11) or in the sugar attached at the 3-position or both. WO 01/79520 demonstrates that the desosaminyl transferase EryCIII exhibits relaxed specificity with respect to the pseudoaglycone substrate, converting 3-*O*-rhamnosyl erythronolides into the corresponding 3-*O*-rhamnosyl erythromycins. Appropriate modified substrates may also be produced by chemical semi-synthetic methods. Alternatively, methods of engineering the erythromycin-producing polyketide synthase, DEBS, to produce modified erythromycins are well known in the art (for example WO 93/13663, WO 98/01571, WO 98/01546, WO 98/49315, Kato, Y. *et al.*, 2002). Likewise, WO 01/79520 describes methods for obtaining erythronolides with alternative sugars attached at the 3-position. Therefore, the term "compounds of the invention" includes all such non-natural aglycone compounds as described previous additionally with alternative sugars at the C-5 position. All these documents are incorporated herein by reference.

It will readily occur to those skilled in the art that the compounds of the invention containing a mycaminosyl moiety at the C-5 position could be modified at the C-4 hydroxyl group of the mycaminosyl moiety, including but not limited to glycosylation (see also WO 01/79520), acylation or chemical modification.

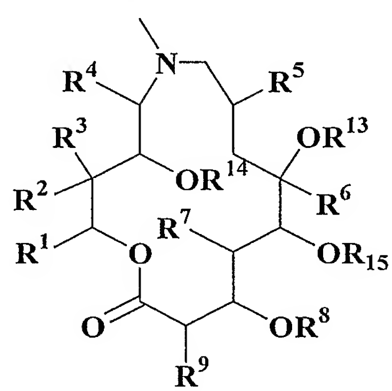
The present invention thus provides variants of erythromycin and related macrolides having at the 5-position a non-naturally occurring sugar, in particular an *O*-mycaminosyl, or *O*-angolosaminyl residue or a derivative or precursor thereof, specifically an *O*-angolosaminyl residue or a derivative thereof.

The term "variants of erythromycin" encompasses (a) erythromycins A, B, C and D; (b) semi-synthetic derivatives such as azithromycin and other derivatives as discussed in EP 1024145, which is incorporated herein by reference; (c) variants produced by genetic engineering and semi-synthetic derivatives thereof. Variants produced by genetic engineering include variants as taught in, or producible by, methods taught in WO 98/01571, EP 1024145, WO 93/13663, WO 98/49315 and WO 01/79520 which are incorporated herein by reference. The compounds of the invention include variants of erythromycin where the natural sugar at position C-5 has been replaced with mycaminose or angolosamine and also includes compounds of the following formulas (I –erythromycins and II - azithromycins) and pharmaceutically acceptable salts thereof. No stereochemistry is shown in Formula I or II as all possibilities are covered, including "natural" stereochemistries (as shown elsewhere in this specification) at some or all positions. In particular, the stereochemistry of any -CH(OH)- group is generally independently selectable.

Formula I:



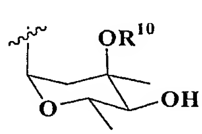
Formula II



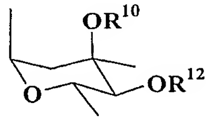
R^1= H, CH_3, C_2H_5 or is selected from i) below;

R^2, R^4, R^5, R^6, R^7 and R^9 are each independently H, OH, CH_3, C_2H_5 or OCH_3;

R^3= H or OH;

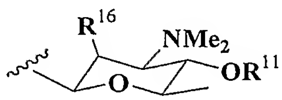
R^8 = H, , rhamnose, 2'-*O*-methyl rhamnose, 2',3'-bis-*O*-methyl rhamnose, 2',3',4'-tri–*O*-methyl rhamnose, oleandrose, oliose, digitoxose, olivose or angolosamine;

R^{10} = H, CH_3 or $C(=O)R_A$, where R_A = C1-C6 alkyl, C2-C6 alkenyl or C2-C6 alkynyl;

R^{11} = H,  , mycarose, C4-*O*-acyl-mycarose or glucose;

R^{12} = H or $C(=O)R_A$, where R_A = C1-C6 alkyl, C2-C6 alkenyl or C2-C6 alkynyl;

R^{13} = H or CH_3;

R^{15} = H or  ;

R^{16} = H or OH;

R^{14} = H or $-C(O)NR^cR^d$ wherein each of R^c and R^d is independently H, C_1-C_{10} alkyl, C_2-C_{20} alkenyl, C_2-C_{10} alkynyl, -$(CH_2)_m(C_6$-C_{10} aryl), or $-(CH_2)_m$(5-10 membered heteroaryl), wherein m is an integer ranging from 0 to 4, and wherein each of the foregoing R^c and R^d groups, except H, may be substituted by 1 to 3 Q groups; or wherein R^c and R^d may be taken together to form a 4-7 membered saturated ring or a 5-10 membered heteroaryl ring, wherein said saturated and heteroaryl rings may include 1 or 2 heteroatoms selected from O, S and N, in addition to the nitrogen to which R^c and R^d are attached, and said saturated ring may include 1 or 2 carbon-carbon double or triple bonds, and said saturated and heteroaryl rings may be substituted by 1 to 3 Q groups; or R^2 and R^{17} taken together form a carbonate ring; each Q is independently selected from halo, cyano, nitro, trifluoromethyl, azido, $-C(O)Q^1$, $-OC(O)Q^1$, $-C(O)OQ^1$, $-OC(O)OQ^1$, $-NQ^2C(O)Q^3$, $-C(O)NQ^2Q^3$, $-NQ^2Q^3$, hydroxy, C_1-C_6 alkyl, C_1-C_6 alkoxy, -$(CH_2)_m(C_6$-C_{10} aryl), and $-(CH_2)_m$(5-10 membered heteroaryl), wherein m is an integer ranging from 0 to 4, and wherein said aryl and heteroaryl substituents may be substituted by 1 or 2 substituents independently selected from halo, cyano, nitro, trifluoromethyl, azido, $-C(O)Q^1$, $-C(O)OQ^1$, $-OC(O)OQ^1$, $-NQ^2C(O)Q^3$, $-C(O)NQ^2Q^3$, $-NQ^2Q^3$, hydroxy, C_1-C_6 alkyl, and C_1-C_6 alkoxy;

each Q^1, Q^2 and Q^3 is independently selected from H, OH, C_1-C_{10} alkyl, C_1-C_6 alkoxy, C_2-C_{10} alkenyl, C_2-C_{10} alkynyl, -(CH_2)m$(C_6$-C_{10} aryl), and $-(CH_2)_m$(5-10 membered heteroaryl), wherein m is an integer ranging from 0 to 4; with the proviso that the compound is not 5-O-dedesosaminyl-5-O-mycaminosyl erythromycin A or D.

The present invention also provides compounds according to formulas I or II above in which:

i) the substituent R^1 is selected from

- an alpha-branched C_3-C_8 group selected from alkyl, alkenyl, alkynyl, alkoxyalkyl and alkylthioalkyl groups any of which may be optionally substituted by one or more hydroxyl groups;
- a C_5-C_8 cycloalkylalkyl group wherein the alkyl group is an alpha-branched C_2-C_5 alkyl group;
- a C_3-C_8 cycloalkyl group or C_5-C_8 cycloalkenyl group, either of which may optionally be substituted by one or more hydroxyl, or one or more C_1-C_4 alkyl groups or halo atoms;

- a 3 to 6 membered oxygen or sulphur containing heterocyclic ring which may be saturated, or fully or partially unsaturated and which may optionally be substituted by one or more C_1-C_4 alkyl groups, halo atoms or hydroxyl groups;
- phenyl which may be optionally substituted with at least one substituent selected from C_1-C_4 alkyl, C_1-C_4 alkoxy and C_1-C_4 alkylthio groups, halogen atoms, trifluoromethyl, and cyano or;
- R^1 is R^{17}-CH_2- where R^{17} is H, C_1-C_8 alkyl, C_2-C_8 alkenyl, C_2-C_8 alkynyl, alkoxyalkyl or alkylthioalkyl containing from 1 to 6 carbon atoms in each alkyl or alkoxy group wherein any of said alkyl, alkoxy, alkenyl or alkynyl groups may be substituted by one or more hydroxyl groups or by one or more halo atoms; or a C_3-C_8 cycloalkyl or C_5-C_8 cycloalkenyl either of which may be optionally substituted by one or more C_1-C_4 alkyl groups or halo atoms; or a 3 to 6 membered oxygen or sulphur containing heterocyclic ring which may be saturated or fully or partially unsaturated and which may optionally be substituted by one or more C_1-C_4 alkyl groups or halo atoms; or a group of the formula SA_{16} wherein A_{16} is C_1-C_8 alkyl, C_2-C_8 alkenyl, C_2-C_8 alkynyl, C_3-C_8 cycloalkyl, C_5-C_8 cycloalkenyl, phenyl or substituted phenyl wherein the substituent is C_1-C_4 alkyl, C_1-C_4 alkoxy or halo, or a 3 to 6 membered oxygen or sulphur-containing heterocyclic ring which may be saturated, or fully or partially unsaturated and which may optionally be substituted by one or more C_1-C_4 alkyl groups or halo atoms;

ii) the –CHOH- at C11 (erythromycins) or C12 (azithromycins) is replaced by a methylene group (-CH2-), a keto group (C=O), or by a 10,11-olefinic bond (erythromycins) or 11,12-olefinic bond (azithromycins);

iii) the substituent R^{11} is H or mycarose or C4-*O*-acyl-mycarose or glucose;

or compounds according to formula I or II above which differ in the oxidation state of one or more of the ketide units (i.e. selection of alternatives from the group: -CO-, -CH(OH)-, alkene –CH-, and CH_2) where the stereochemistry of any -CH(OH)- is also independently selectable, with the proviso that the compounds are not selected from the group consisting of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin D and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin.

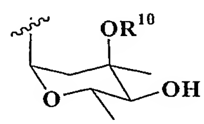
Novel 5-*O*-dedesosaminyl-5-*O*-angolosaminyl erythromycins and azithromycins made available by this aspect of the invention include, but are not limited to those where in the R^{15} group $R^{11} = R^{16} = H$, with the proviso that they are not angolamycin or medermycin (Kinumaki and Suzuki, 1972; Ichinose *et al.*, 2003).

In a preferred embodiment the present invention provides a compound according to formula I or II where:

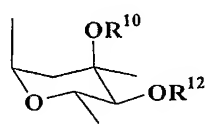
R^1= H, CH_3, C_2H_5 or selected from: an alpha-branched C_3-C_8 group selected from alkyl, alkenyl, alkynyl, alkoxyalkyl and alkylthioalkyl groups any of which may be optionally substituted by one or more hydroxyl groups; a C_5-C_8 cycloalkylalkyl group wherein the alkyl group is an alpha-branched C_2-C_5 alkyl group; a C_3-C_8 cycloalkyl group or C_5-C_8 cycloalkenyl group, either of which may optionally be substituted by one or more hydroxyl, or one or more C_1-C_4 alkyl groups or halo atoms; a 3 to 6 membered oxygen or sulphur containing heterocyclic ring which may be saturated, or fully or partially unsaturated and which may optionally be substituted by one or more C_1-C_4 alkyl groups, halo atoms or hydroxyl groups; phenyl which may be optionally substituted with at least one substituent selected from C_1-C_4 alkyl, C_1-C_4 alkoxy and C_1-C_4 alkylthio groups, halogen atoms, trifluoromethyl, and cyano or R^1 is R^{17}-CH_2- where R^{17} is H, C_1-C_8 alkyl, C_2-C_8 alkenyl, C_2-C_8 alkynyl, alkoxyalkyl or alkylthioalkyl containing from 1 to 6 carbon atoms in each alkyl or alkoxy group wherein any of said alkyl, alkoxy, alkenyl or alkynyl groups may be substituted by one or more hydroxyl groups or by one or more halo atoms; or a C_3-C_8 cycloalkyl or C_5-C_8 cycloalkenyl either of which may be optionally substituted by one or more C_1-C_4 alkyl groups or halo atoms; or a 3 to 6 membered oxygen or sulphur containing heterocyclic ring which may be saturated or fully or partially unsaturated and which may optionally be substituted by one or more C_1-C_4 alkyl groups or halo atoms; or a group of the formula SA_{16} wherein A_{16} is C_1-C_8 alkyl, C_2-C_8 alkenyl, C_2-C_8 alkynyl, C_3-C_8 cycloalkyl, C_5-C_8 cycloalkenyl, phenyl or substituted phenyl wherein the substituent is C_1-C_4 alkyl, C_1-C_4 alkoxy or halo, or a 3 to 6 membered oxygen or sulphur-containing heterocyclic ring which may be saturated, or fully or partially unsaturated and which may optionally be substituted by one or more C_1-C_4 alkyl groups or halo atoms

R^2, R^4, R^5, R^6, R^7 and R^9 are all CH_3

R^3 is H or OH

R^8 = H or  or is selected from rhamnose, 2'-*O*-methyl rhamnose, 2',3'-bis-*O*-methyl rhamnose, 2',3',4'-tri-*O*-methyl rhamnose, oleandrose, oliose, digitoxose, olivose and angolosamine;

R10 = H or CH3

R^{11} = H or 

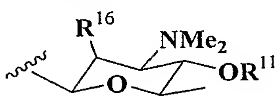
R^{12}= H or C(=O)R_A, where R_A = C1-C6 alkyl, C2-C6 alkenyl or C2-C6 alkynyl

R^{13}= H or CH_3

R^{14} = H or –C(O)NR^cR^d wherein each of R^c and R^d is independently H, C_1-C_{10} alkyl, C_2-C_{20} alkenyl, C_2-C_{10} alkynyl, -$(CH_2)_m$(C_6-C_{10} aryl), or –$(CH_2)_m$(5-10 membered heteroaryl), wherein m is an integer ranging from 0 to 4, and wherein each of the foregoing R^c and R^d groups, except H, may be substituted by

1 to 3 Q groups; or wherein R^c and R^d may be taken together to form a 4-7 membered saturated ring or a 5-10 membered heteroaryl ring, wherein said saturated and heteroaryl rings may include 1 or 2 heteroatoms selected from O, S and N, in addition to the nitrogen to which R^c and R^d are attached, and said saturated ring may include 1 or 2 carbon-carbon double or triple bonds, and said saturated and heteroaryl rings may be substituted by 1 to 3 Q groups; or R^2 and R^{17} taken together form a carbonate ring; each Q is independently selected from halo, cyano, nitro, trifluoromethyl, azido, $-C(O)Q^1$, $-OC(O)Q^1$, $-C(O)OQ^1$, $-OC(O)OQ^1$, $-NQ^2C(O)Q^3$, $-C(O)NQ^2Q^3$, $-NQ^2Q^3$, hydroxy, C_1-C_6 alkyl, C_1-C_6 alkoxy, $-(CH_2)_m(C_6$-C_{10} aryl), and $-(CH_2)_m$(5-10 membered heteroaryl), wherein m is an integer ranging from 0 to 4, and wherein said aryl and heteroaryl substituents may be substituted by 1 or 2 substituents independently selected from halo, cyano, nitro, trifluoromethyl, azido, $-C(O)Q^1$, $-C(O)OQ^1$, $-OC(O)OQ^1$, $-NQ^2C(O)Q^3$, $-C(O)NQ^2Q^3$, $-NQ^2Q^3$, hydroxy, C_1-C_6 alkyl, and C_1-C_6 alkoxy;

each Q^1, Q^2 and Q^3 is independently selected from H, OH, C_1-C_{10} alkyl, C_1-C_6 alkoxy, C_2-C_{10} alkenyl, C_2-C_{10} alkynyl, $-(CH_2)m(C_6$-C_{10} aryl), and $-(CH_2)_m$(5-10 membered heteroaryl), wherein m is an integer ranging from 0 to 4; with the proviso that the compound is not 5-O-dedesosaminyl-5-O-mycaminosyl erythromycin A or D

R^{15} = H or 

R^{16} = H or OH

with the proviso that the compounds are not selected from the group consisting of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin D and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin

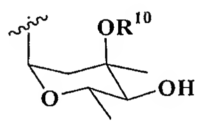
In a further preferred embodiment the present invention provides a compound according to formula I, wherein:

R^1= H, CH_3, C_2H_5 or selected from: an alpha-branched C_3-C_8 group selected from alkyl, alkenyl, alkynyl, alkoxyalkyl and alkylthioalkyl groups any of which may be optionally substituted by one or more hydroxyl groups; a C_5-C_8 cycloalkylalkyl group wherein the alkyl group is an alpha-branched C_2-C_5 alkyl group; a C_3-C_8 cycloalkyl group or C_5-C_8 cycloalkenyl group, either of which may optionally be substituted by one or more hydroxyl, or one or more C_1-C_4 alkyl groups or halo atoms; a 3 to 6 membered oxygen or sulphur containing heterocyclic ring which may be saturated, or fully or partially unsaturated and which may optionally be substituted by one or more C_1-C_4 alkyl groups, halo atoms or hydroxyl groups; phenyl which may be optionally substituted with at least one substituent selected from C_1-C_4 alkyl, C_1-C_4 alkoxy and C_1-C_4 alkylthio groups, halogen atoms, trifluoromethyl, and cyano or R^1 is R^{17}-CH_2- where R^{17} is H, C_1-C_8 alkyl, C_2-C_8 alkenyl, C_2-C_8 alkynyl, alkoxyalkyl or alkylthioalkyl containing from 1 to 6 carbon atoms in each alkyl or alkoxy group wherein any of said alkyl, alkoxy, alkenyl or alkynyl groups may be substituted by one or more hydroxyl groups or by one or more halo atoms; or a

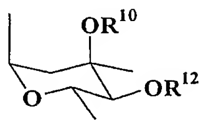
C_3-C_8 cycloalkyl or C_5-C_8 cycloalkenyl either of which may be optionally substituted by one or more C_1-C_4 alkyl groups or halo atoms; or a 3 to 6 membered oxygen or sulphur containing heterocyclic ring which may be saturated or fully or partially unsaturated and which may optionally be substituted by one or more C_1-C_4 alkyl groups or halo atoms; or a group of the formula SA_{16} wherein A_{16} is C_1-C_8 alkyl, C_2-C_8 alkenyl, C_2-C_8 alkynyl, C_3-C_8 cycloalkyl, C_5-C_8 cycloalkenyl, phenyl or substituted phenyl wherein the substituent is C_1-C_4 alkyl, C_1-C_4 alkoxy or halo, or a 3 to 6 membered oxygen or sulphur-containing heterocyclic ring which may be saturated, or fully or partially unsaturated and which may optionally be substituted by one or more C_1-C_4 alkyl groups or halo atoms

R^2, R^4, R^5, R^6, R^7 and R^9 are all CH_3

R^3 is H or OH

R^8 = H or  or is selected from rhamnose, 2'-*O*-methyl rhamnose, 2',3'-bis-*O*-methyl rhamnose, 2',3',4'-tri-*O*-methyl rhamnose, oleandrose, oliose, digitoxose, olivose and angolosamine;

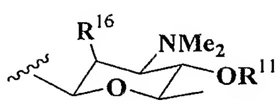
R10 = H or CH3

R^{11} = H or 

R^{12}= H or $C(=O)R_A$, where R_A = C1-C6 alkyl, C2-C6 alkenyl or C2-C6 alkynyl

R^{13}= H or CH_3

R^{14} = H

R^{15} = H or 

R^{16} = H or OH

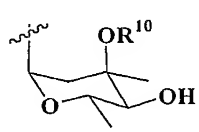
with the proviso that the compounds are not selected from the group consisting of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin D and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin

In a more preferred embodiment the present invention provides a compound according to formula I where:

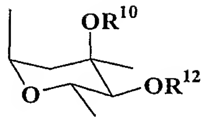
R^1= C_2H_5 optionally substituted with a hydroxyl group

R^2, R^4, R^5, R^6, R^7 and R^9 are all CH_3

R^3 is H or OH

R^8 = H or  ;

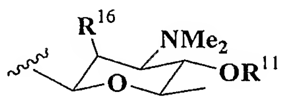
R^{10} = H or CH_3

R^{11} = H or 

R^{12}= H or C(=O)R_A, where R_A = C1-C6 alkyl, C2-C6 alkenyl or C2-C6 alkynyl

R^{13}= H or CH_3

R^{14} = H

R^{15} = H or 

R^{16} = H or OH

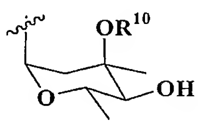
with the proviso that the compounds are not selected from the group consisting of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin D

In a more preferred embodiment the present invention provides a compound according to formula I where:

R^1= C_2H_5 optionally substituted with a hydroxyl group

R^2, R^4, R^5, R^6, R^7 and R^9 are all CH_3

R^3 is H or OH

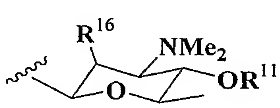
R^8 = H or  ;

R^{10} = H or CH_3

R^{12}= H

R^{13}= H or CH_3

R^{14} = H

R^{15} = H or 

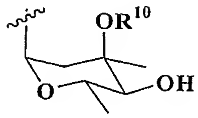
R^{16} = H or OH

In a highly preferred embodiment the present invention provides a compound according to formula I where:

R^1= C_2H_5

R^2, R^4, R^5, R^6, R^7 and R^9 are all CH_3

R^3 is H or OH

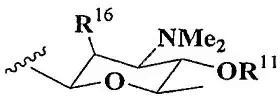
R^8 = H or ;

R^{10} = H or CH_3

R^{12}= H

R^{13}= H or CH_3

R^{14} = H

R^{15} = H or 

R^{16} = H or OH

with the proviso that the compounds are not selected from the group consisting of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin D.

Additionally, a person of skill in the art will appreciate that, using the methods of the present invention, mycaminose and angolosamine may be added to other aglycones or pseudoaglycones for example (but without limitation) a tylactone or spinosyn pseudoaglycone. These other aglycones or pseudoaglycones may be the naturally occurring structure or they may be modified in the aglycone backbone, such modified substrates may be produced by chemical semi-synthetic methods (Kaneko *et al.*, 2000 and references cited therein). or, alternatively, via PKS engineering, such methods are well known in the art (for example WO 93/13663, WO 98/01571, WO 98/01546, WO 98/49315, Kato, Y. *et al.*, 2002). Therefore, in a further embodiment the present invention provides 5-*O*-angolosaminyl tylactone, 5-*O*-mycaminosyl tylactone, 17-*O*-angolosaminyl spinosyn and 17-*O*-mycaminosyl spinosyn.

Moreover, the process of the host cell selection further comprises the optional step of deleting or inactivating or adding or manipulating genes in the host cell. This process comprises the improvement of recombinant host strains for the preparation and isolation of compounds of the invention, in particular 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycins and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycins, specifically 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin C, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin B, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin D and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin. This approach is exemplified in Example 1 by introducing an *eryBVI* mutation into the chromosome of *S. erythraea* SGQ2 in order to optimise the conversion of the substrate 3-*O*-mycarosyl erythronolide B to 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycins.

In a further aspect the invention relates to the construction of gene cassettes. The cloning method used to isolate these gene cassettes is analogous to that used in PCT/GB03/003230 and diverges significantly from the approach previously described (WO 01/79520) by assembling the gene cassette directly in an expression vector rather than pre-assembling the genes in pUC18/19 plasmids, thus

providing a more rapid cloning procedure for the isolation of gene cassettes. The strategy for isolating these gene cassettes is exemplified in Example 1 to Example 11. A schematic overview of the strategy is given in Figure 2.

Another aspect of the invention allows the enhancement of gene expression by changing the order of genes in a gene cassette, the genes including but not limited to *tylMI, tylMIII, tylB, eryCVI, tylAI, tylAII, eryCIII, eryBV, angAI, angAII, angMIII, angB, angMI, angorf14, angorf4, eryBVI, eryK, eryG, angMII, tylMII, desVII,,midI, spnO, spnN, spnP* and genes with similar functions, allowing the arrangement of the genes in a multitude of permutations (Figure 2).

The cloning strategy outlined in this invention also allows the introduction of a histidine tag in combination with a terminator sequence 3' of the gene cassette to enhance gene expression (see Example 1). Those skilled in the art will appreciate other terminator sequences well known in the art could be used. See, for example Bussiere and Bastia (1999), Bertram *et al.* (2001) and Kieser *et al.* (2000), incorporated herein by reference.

Another aspect of the invention comprises the use of alternative promoters such as P*tipA* (Ali *et al.*, 2002) and/or P*ptr* (Salah-Bey *et al.*, 1995) to express genes and/or assembled gene cassette(s) to enhance expression.

Another aspect of the invention describes the multiple uses of promoter sequences in the assembled gene cassette to enhance gene expression as exemplified in Example 6.

Another aspect of the invention describes the addition of genes encoding for a NDP-glucose-synthase such as *tylAI* and a NDP-glucose-4,6-dehydratase such as *tylAII* to the gene cassette in order to enhance the endogenous production of the activated sugar substrate. Those skilled in the art will appreciate that alternative sources of equivalent sugar biosynthetic pathway genes may be used. In this context alternative sources include but are not limited to:

<u>TylAI- homologues</u>: DesIII of *Streptomyces venezuelae* (accession no AAC68682), GrsD of *Streptomyces griseus* (accession no AAD31799), AveBIII of *Streptomyces avermitilis* (accession no BAA84594), Gtt of *Saccharopolyspora spinosa* (accession no AAK83289), SnogJ of *Streptomyces nogalater* (accession no AAF01820), AclY of *Streptomyces galilaeus* (accession no BAB72036), LanG of *Streptomyces cyanogenus* (accession no AAD13545), Graorf16(GraD) of *Streptomyces violaceoruber* (accession no AAA99940), OleS of *Streptomyces antibioticus* (accession no AAD55453) and StrD of *Streptomyces griseus* (accession no A26984) and AngAI of *S. eurythermus*.

<u>TylAII- homologues</u>: AprE of *Streptomyces tenebrarius* (accession no AAG18457), GdH of *S. spinosa* (accession no AAK83290), DesIV of *S. venezuelae* (accession no AAC68681), GdH of *S. erythraea* (accession no AAA68211), AveBII of *S. avermitilis* (accession no BAA84593), Scf81.08C of *Streptomyces coelicolor* (accession no CAB61555), LanH of *S. cyanogenus*

(accession no AAD13546), Graorf17 (GraE) of *S. violaceoruber* (accession no S58686), OleE of *S. antibioticus* (accession no AAD55454), StrE of *S. griseus* (accession no P29782) and AngAII of *S. eurythermus*.

Similarly, alternative sources for activated sugar biosynthesis gene homologues to *tylMIII, angAIII, eryCII, tylMII, angMII, tylB, angB, eryCI, tylMI, angMI, eryCVI, tylIa, angorf14, angorf4, spnO, eryBVI, eryBV, eryCIII, desVII, midI, spnN and spnP* will readily occur to those skilled in the art, and can be used.

Another aspect of the invention describes the use of alternative glycosyltransferases in the gene cassettes such as EryCIII. Those skilled in the art will appreciate that alternative glycosyltransferases may be used. In this context alternative glycosyltransferases include but are not limited to: TylMII (Accession no CAA57472), DesVII (Accession noAAC68677), MegCIII (Accession no AAG13921), MegDI (Accession no AAG13908) or AngMII of *S. eurythermus*.

In one aspect of the present invention, the gene cassette may additionally comprise a chimeric glycosyltransferase (GT). This is particularly of benefit where the natural GT does not recognise the combination of sugar and aglycone that is required for the synthesis of the desired analogue. Therefore, in this aspect the present invention specifically contemplates the use of a chimearic GT wherein part of the GT is specific for the recognition of the sugar whose synthesis is directed by the genes in said expression cassette when expressed in an appropriate strain background and part of the GT is specific for the aglycone or pseudoaglycone template (Hu and Walker, 2002).

Those skilled in the art will appreciate that different strategies may be used for the introduction of gene cassettes into the host strain, such as site-specific integration vectors (Smovkina *et al.*, 1990; Lee *et al.*, 1991; Matsuura *et al.*, 1996; Van Mellaert *et al.*, 1998; Kieser *et al.*, 2000). Alternatively, plasmids containing the gene cassettes may be integrated into any neutral site on the chromosome using homologous recombination sites. Further, for a number of actinomycete host strains, including *S. erythraea,* the gene cassettes may be introduced on self-replicating plasmids (Kieser *et al.*, 2000; WO 98/01571).

A further aspect of the invention provides a process for the production of compounds of the invention and optionally for the isolation of said compounds.

A further aspect of the invention is the use of different fermentation methods to optimise the production of the compounds of the invention as exemplified in Example 1. Another aspect of the invention is the addition of *ery* genes such as *eryK* and/or *eryG* into the gene cassette. One skilled in the art will appreciate that the process can be optimised for the production of a specific erythromycin (i.e. A, B, C, D) or azithromycin by manipulation of the genes *eryG* (responsible for the methylation on the mycarose sugar) and/or *eryK* (responsible for hydroxylation at C12). Thus, to optimise the production of the A-form, an extra copy of *eryK* may be included into the gene cassette. Conversely, if the

erythromycin B analogue is required, this can be achieved by deletion of the *eryK* gene from the *S. erythraea* host strain, or by working in a heterologous host in which the gene and/or its functional homologue, is not present. Similarly, if the erythromycin D analogue is required, this can be achieved by deletion of both *eryG* and *eryK* genes from the *S. erythraea* host strain, or by working in a heterologous host in which both genes and/or their functional homologues are not present. Similarly, if the erythromycin C analogue is required, this can be achieved by deletion of the *eryG* gene from the *S. erythraea* host strain, or by working in a heterologous host in which the gene and/or its functional homologues are not present.

In this context a preferred host cell strain is a mammalian cell strain, fungal cells strain or a prokaryote. More preferably the host cell strain is an actinomycete, a Pseudomonad, a myxobacterium or an *E. coli*. In a more preferred embodiment the host cell strain is an actinomycete, still more preferably including, but not limited to *Saccharopolyspora erythraea*, *Streptomyces coelicolor*, *Streptomyces avermitilis*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces fradiae*, *Streptomyces eurythermus*, *Streptomyces longisporoflavus*, *Streptomyces hygroscopicus*, *Saccharopolyspora spinosa*, *Micromonospora griseorubida*, *Streptomyces lasaliensis*, *Streptomyces venezuelae*, *Streptomyces antibioticus*, *Streptomyces lividans*, *Streptomyces rimosus*, *Streptomyces albus*, *Amycolatopsis mediterranei*, *Nocardia sp*, *Streptomyces tsukubaensis* and *Actinoplanes sp. N902-109*. In a still more preferred embodiment the host cell strain is selected from *Saccharopolyspora erythraea*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces albus*, *Streptomyces lividans*, *Streptomyces hygroscopicus sp.*, *Streptomyces hygroscopicus var. ascomyceticus*, *Streptomyces longisporoflavus*, *Saccharopolyspora spinosa*, *Streptomyces tsukubaensis*, *Streptomyces coelicolor*, *Streptomyces fradiae*, *Streptomyces rimosus*, *Streptomyces avermitilis*, *Streptomyces eurythermus*, *Streptomyces venezuelae*, *Amycolatopsis mediterranei*. In the most highly preferred embodiment the host strain is *Saccharopolyspora erythraea*.

The present invention provides methods for the production and isolation of compounds of the invention, in particular of erythromycin and azithromycin analogues which differ from the natural compound in the glycosylation of the C-5 position, for example but without limitation: novel 5-*O*-dedesosaminyl-5-*O*-mycaminosyl or angolosaminyl erythromycins and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl, or angolosaminyl azithromycins which are useful as anti-microbial agents for use in human or animal health.

In further aspects the present invention provides novel products as obtainable by any of the processes disclosed herein.

Brief description of Figures

Figure 1A: Structures of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A, 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin B and 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin C.

Figure 1B: Structure of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin.

Figure 2: Schematic overview over the gene cassette cloning strategy. Vector pSG144 was derived from vector pSG142 (Gaisser *et al.*, 2000). Abbreviations: *dam*$^-$: DNA isolated from *dam*$^-$ strain background, *Xba*I^{met}: *Xba*I site sensitive to Dam methylation, *ery*RHS: DNA fragment of the right hand side of the *ery*-cluster as described previously (Gaisser *et al.*, 2000).

Figure 3: Amino acid comparison between the published sequence of TylA1 (below, SEQ ID NO: 1) and the amino acid sequence detected from the sequencing data described in this invention (above, SEQ ID NO: 2). The changes in the amino acid sequence are underlined.

Figure 4: Amino acid comparison between the published sequence of TylAII (below, SEQ ID NO: 3) and the amino acid sequence detected from the sequencing data described in this invention (above, SEQ ID NO: 4). The changes in the amino acid sequence are underlined.

Figure 5: Structure of 5-*O*-angolosaminyl tylactone.

Figure 6: Shows an overview of the angolamycin polyketide synthase gene cluster.

Figure 7: The DNA sequence which comprises *orf14* and *orf15 (angB)* from the angolamycin gene cluster (SEQ ID NO: 5).

Figure 8: The DNA sequence which comprises *orf2 (angAI)*, *orf3 (angAII)* and *orf4* from the angolamycin gene cluster (SEQ ID NO: 6).

Figure 9: The DNA sequence which comprises *orf1* (angMIII)*, *orf2* (angMII)*, and *orf3* (angMI)* from the angolamycin gene cluster (SEQ ID NO: 7).

Figure 10: The amino acid sequence which corresponds to *orf2* (*angAI*, SEQ ID NO: 8).

Figure 11: The amino acid sequence which corresponds to *orf3* (*angAII*, SEQ ID NO: 9).

Figure 12: The amino acid sequence which corresponds to *orf4* (SEQ ID NO: 10)

Figure 13: The amino acid sequence which corresponds to *orf14* (SEQ ID NO: 11).

Figure 14: The amino acid sequence which corresponds to *orf15* (*angB*, SEQ ID NO: 12).

Figure 15: The amino acid sequence which corresponds to *orf1** (*angMIII*, SEQ ID NO: 13).

Figure 16: The amino acid sequence which corresponds to *orf2** (*angMII,* SEQ ID NO: 14).

Figure 17: The amino acid sequence which corresponds to *orf3** (*angMI*, SEQ ID NO: 15).

General Methods

Escherichia coli XL1-Blue MR (Stratagene), *E. coli* DH10B (GibcoBRL) and *E. coli* ET12567 were grown in 2xTY medium as described by Sambrook *et al.*, (1989). Vector pUC18, pUC19 and Litmus 28 were obtained from New England Biolabs. *E. coli* transformants were selected with 100 μg/mL ampicillin. Conditions used for growing the *Saccharopolyspora erythraea* NRRL 2338-red variant strain were as described previously (Gaisser *et al.*, 1997, Gaisser *et al.*, 1998). Expression vectors in *S. erythraea* were derived from plasmid pSG142 (Gaisser *et al.*, 2000). Plasmid-containing *S. erythraea* were selected with 25-40 μg/mL thiostrepton or 50 μg/mL apramycin. To investigate the production of antibiotics, *S. erythraea* strains were grown in sucrose-succinate medium (Caffrey *et al.*, 1992) as described previously (Gaisser *et al.*, 1997) and the cells were harvested by centrifugation. Chromosomal DNA of *Streptomyces rochei* ATCC21250 was isolated using standard procedures (Kieser *et al.*, 2000). Feedings of 3-*O*-mycarosyl erythronolide B or tylactone were carried out at concentrations between 25 to 50 mg /L.

DNA manipulation and sequencing

DNA manipulations, PCR and electroporation procedures were carried out as described in Sambrook *et al.*, (1989). Protoplast formation and transformation procedures of *S. erythraea* were as

described previously (Gaisser *et al.*, 1997). Southern hybridizations were carried out with probes labelled with digoxigenin using the DIG DNA labelling kit (Boehringer Mannheim). DNA sequencing was performed as described previously (Gaisser *et al.*, 1997), using automated DNA sequencing on double stranded DNA templates with an ABI Prism 3700 DNA Analyzer. Sequence data were analysed using standard programs.

Extraction and mass spectrometry

1 mL of each fermentation broth was harvested and the pH was adjusted to pH 9. For extractions an equal volume of ethyl acetate, methanol or acetonitrile was added, mixed for at least 30 min and centrifuged. For extractions with ethyl acetate, the organic layer was evaporated to dryness and then re-dissolved in 0.5 mL methanol. For methanol and acetonitrile extractions, supernatant was collected after centrifugation and used for analysis. High resolution spectra were obtained on a Bruker BioApex II FT-ICR (Bruker, Bremen, FRG).

Analysis of culture broths

An aliquot of whole broth (1 mL) was shaken with CH_3CN (1 mL) for 30 minutes. The mixture was clarified by centrifugation and the supernatant analysed by LCMS. The HPLC system comprised an Agilent HP1100 equipped with a Luna 5 μm C18 BDS 4.6 × 250 mm column (Phenomenex, Macclesfield, UK) heated to 40 °C. The gradient elution was from 25% mobile phase B to 75% mobile phase B over 19 minutes at a flow rate of 1 mL/min. Mobile phase A was 10% acetonitrile: 90% water, containing 10 mM ammonium acetate and 0.15% formic acid, mobile phase B was 90% acetonitrile:10% water, containing 10 mM ammonium acetate and 0.15% formic acid. The HPLC system described was coupled to a Bruker Daltonics Esquire3000 electrospray mass spectrometer operating in positive ion mode.

Extraction and purification protocol:

For NMR analysis of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A the fermentation broth was clarified by centrifugation to provide supernatant and cells. The supernatant was applied to a column (16 × 15 cm) of Diaion® HP20 resin (Supelco), washed with 10% Me_2CO/H_2O (2 × 2 L) and then eluted with Me_2CO (3.5 L). The cells were mixed to homogeneity with an equal volume of Me_2CO/MeOH (1:1). After at least 30 minutes the slurry was clarified by centrifugation and the supernatant decanted. The pelleted cells were similarly extracted once more with Me_2CO/MeOH (1:1). The cell extracts were combined with the Me_2CO from the HP20 column and the solvent was removed *in vacuo* to give an aqueous concentrate. The aqueous was extracted with EtOAc (3 ×) and the solvent removed *in vacuo* to give a crude extract. The residue was dissolved in CH_3CN/MeOH and purified by repeated rounds of reverse phase (C18) high performance liquid chromatography using a Gilson HPLC,

eluting a Phenomenex 21.2 × 250 mm Luna 5 μm C18 BDS column at 21 mL/min. Elution with a linear gradient of 32.5% B to 63% B was used to concentrate the macrolides followed by isocratic elution with 30% B to resolve the individual erythromycins. Mobile phase A was 20 mM ammonium acetate and mobile phase B was acetonitrile.
High resolution mass spectra were acquired on a Bruker BioApex II FTICR (Bruker, Bremen, Germany).

For NMR analysis of 5-*O*-angolosaminyl tylactone bioconversion experiments were performed as previously described with four 2 L flasks containing each 400 mL of SSDM medium inoculated with 5% of pre-cultures. Feedings with tylactone were carried out at 50 mg/L. The culture was centrifuged and the pH of the supernatant was adjusted to about pH 9 followed by extractions with three equal volumes of ethyl acetate. The cell pellet was extracted twice with equal volumes of a mixture of acetone-methanol (50:50, vol/vol). The extracts were combined and concentrated *in vacuo*. The resulting aqueous fraction was extracted three times with ethyl acetate and the extracts were combined and evaporated until dryness. This semi purified extract was dissolved in methanol and purified by preparative HPLC on a Gilson 315 system using a 21 mm × 250 mm Prodigy ODS3 column (Phenomenex, Macclesfield, UK). The mobile phase was pumped at a flow rate of 21 mL/min as a binary system consisting of 30% CH_3CN, 70% H_2O increasing linearly to 70% CH_3CN over 20 min.

Sequence Information

Table I – Sequence information for the angolosamine biosynthetic genes included in the gene cassettes

Gene (named according to tyl equivalent)	**Bases in Figure**	**Corresponding polypeptide Figure number**
orf2 (*angAI*)	14847-15731c from Figure 8 (SEQ ID NO: 6)	Figure 10 (SEQ ID NO: 8) NDP-hexose synthase
orf3 (*angAII*)	13779-14774c from Figure 8 (SEQ ID NO: 6)	Figure 11 (SEQ ID NO: 9) NDP-hexose 4,6-dehydratase
orf4 (N-part) (C-part)	11306-13666c from Figure 8 (SEQ ID NO: 6)	Figure 12 (SEQ ID NO: 10) typeII thioesterase NDP-hexose 2,3-dehydratase
orf14	1162-2160c from Figure 7 (SEQ ID NO: 5)	Figure 13 (SEQ ID NO: 11) NDP-hexose 4-ketoreductase
orf15 (*angB*)	33-1151c from Figure 7 (SEQ ID NO: 5)	Figure 14 (SEQ ID NO: 12) NDP-hexoseaminotransferase
*orf1** (*angMIII*)	59800-61140 from Figure 9 (SEQ ID NO: 7)	Figure 15 (SEQ ID NO: 13) Hypothetical NDP hexose 3,4

Gene (named according to tyl equivalent)	Bases in Figure	Corresponding polypeptide Figure number
		isomerase
*orf2** (*angMII*)	61159-62430 from Figure 9 (SEQ ID NO: 7)	Figure 16 (SEQ ID NO: 14) angolosaminyl glycosyl transferase
*orf3** (*angMI*)	62452-63171 from Figure 9 (SEQ ID NO: 7)	Figure 17 (SEQ ID NO: 15) N,N-dimethyl transferase

Note : c indicates that the gene is encoded by the complement DNA strand
potential functions of the predicted polypeptides (SEQ ID No.8 to 15) were obtained from the NCBI database using a BLAST search.

Example 1: Bioconversion of 3-*O*-mycarosyl erythronolide B to 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycins using gene cassette pSG144*tylAItylAIItylMIIItylBtylIatylMIeryCIII*.

Isolation of pSG143

Plasmid pSG142 (Gaisser *et al.*, 2000) was digested with *Xba*I and a fill-in reaction was performed using standard protocols. The DNA was re- ligated and used to transform *E. coli* DH10B. Construct pSG143 was isolated and the removal of the *Xba*I site was confirmed by sequence analysis.

Isolation of pUC18eryBVcas

The gene *eryBV* was amplified by PCR using the primers casOleG21 (WO01/79520) and 7966 5'-GGGGAATTC<u>AGATCT</u>GG<u>TCTAGA</u>GGTCAGCCGGCGTGGCGGCGCGTGAGTTCCTCCAGTCGCGGGACGATCT -3' (SEQ ID NO: 16) and pSG142 (Gaisser *et al.*, 2000) as template. The PCR fragment was cloned using standard procedures and plasmid pUC18eryBVcas was isolated with an *Nde*I site overlapping the start codon of *eryBV* and *Xba*I and *Bgl*II sites (underlined) following the stop codon. The construct was verified by sequence analysis.

Isolation of vector pSGLit1

The isolation of this vector is described in PCT/GB03/003230.

Isolation of pSGLit1eryCIII

Plasmid pSGCIII (WO01/79520) was digested with *Nde*I/*Bgl*II and the insert fragment was isolated and ligated with the *Nde*I/*Bgl*II treated vector fragment of pSGLit1. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit1*eryCIII* was isolated using standard procedures. The

construct was confirmed using restriction digests and sequence analysis. This cloning strategy allows the introduction of a *his*-tag C-terminal of EryCIII.

Isolation of pSGLit1tylMII

Plasmid pSGTYLM2 (WO01/7952) was digested with *Nde*I/*Bgl*II and the insert fragment was isolated and ligated with the *Nde*I/*Bgl*II treated vector fragment of pSGLit1. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit1*tylMII* was isolated using standard procedures. The construct was confirmed using restriction digests and sequence analysis. This cloning strategy allows the introduction of a *his*-tag C-terminal of TylMII.

Isolation of pSG144

Plasmid pSGLit1 was isolated and digested with *Nde*I/*Bgl*II and an approximately 1.3 kb insert was isolated. Plasmid pSG143 was digested with *Nde*I/*Bgl*II, the vector band was isolated and ligated with the approximately 1.3 kb band from pSGLit1 followed by transformation of *E. coli* DH10B. Plasmid pSG144 (Figure 2) was isolated and the construct was verified by DNA sequence analysis. This vector allows the assembly of gene cassettes directly in an expression vector (Figure 2) without prior assembly in pUC-derived vectors (WO 01/79520) in analogy to PCT/GB03/003230 using vector pSG144 instead of pSGset1. Plasmid pSG144 differs from pSG142 in that the *Xba*I site between the thiostrepton resistance gene and the eryRHS has been deleted and the *his*- tag at the end of *eryBV* has been removed from pSG142 and replaced in pSG144 with an *Xba*I site at the end of *eryBV*. This is to facilitate direct cloning of genes to replace *eryBV* and then build up the cassette.

Isolation of pSG144eryCIII

EryCIII was amplified by PCR reaction using standard protocols, with primers casOleG21 (WO 01/79520) and caseryCIII2 (WO 01/79520) and plasmid pSGCIII (Gaisser *et al*., 2000) as template. The approximately 1.3 kb PCR product was isolated and cloned into pUC18 using standard techniques. Plasmid pUCCIIIcass was isolated and the sequence was verified. The insert fragment of plasmid pUCCIIIcass was isolated after *Nde*I/*Xba*I digestion and ligated with the *Nde*I/*Xba*I digested vector fragment of pSG144. After the transformation of *E. coli* DH10B plasmid pSG144*eryCIII* was isolated using standard techniques.

Isolation of pUC19tylAI

Primers BIOSG34 5'-GGGCATATGAACGACCGTCCCCGCCGCGCCATGAAGGG- 3' (SEQ ID NO: 17) and 5'-CCCCTCTAGAGGTCACTGTGCCCGGCTGTCGGCGGCGGCCCCGCGCATGG-3' (SEQ ID NO: 18) were used with genomic DNA of *Streptomyces fradiae* as template to amplify *tylAI*.

The amplified product was cloned using standard protocols and plasmid pUC19*tylAI* was isolated. The insert was verified by DNA sequence analysis. Differences to the published sequence are shown in Figure 3.

Isolation of pSGLit2

Plasmid Litmus 28 was digested with *Spe*I/*Xba*I and the vector fragment was isolated. Plasmid pSGLit1 (*dam*$^-$) was digested with *Xba*I and the insert band was isolated and ligated with the *Spe*I/*Xba*I digested vector fragment of Litmus 28 followed by the transformation of *E. coli* DH10B using standard techniques. Plasmid pSGLit2 was isolated and the construct was verified by restriction digest and sequence analysis. This plasmid can be used to add a 5' region containing an *Xba*I site sensitive to Dam methylation and a Shine Dalgarno region thus converting genes which were originally cloned with an *Nde*I site overlapping the start codon and an *Xba*I site 3' of the stop codon for the assembly of gene cassettes. This conversion includes the transformation of the ligations into *E. coli* ET12567 followed by the isolation of *dam*$^-$ DNA and *Xba*I digests. Examples for this strategy are outlined below.

Isolation of pSGLit2tylAI

Plasmid pSGLit2 and pUC19*tylAI* were digested with *Nde*I / *Xba*I and the insert band of pUC19*tylAI* and the vector band of pSGLit2 were isolated, ligated and used to transform *E. coli* ET12567. Plasmid pSGLit2*tylAI* (*dam*$^-$) was isolated.

Isolation of pUC19tylAII

Primers 5'-CCCC<u>TCTAGA</u>GGTCATGCGCGCTCCAGTTCCCTGCCGCCCGGGGACCGC TTG- 3' (SEQ ID NO: 19) and 5' –GGG<u>TCTAGA</u>TCGATTAATTAAGGAGGACATTCATGCGCGT CCTGGTGACCGGAGGTGCGGGCTTCATCGGCTCGCACTTCA- 3' (SEQ ID NO: 20) and genomic DNA of *Streptomyces fradiae* as template were used for a PCR reaction applying standard protocols to amplify *tylAII*. The approximately 1 kb sized DNA fragment was isolated and cloned into *Sma*I-cut pUC19 using standard techniques. The DNA sequencing of this construct revealed that 12 nucleotides at the 5' end had been removed possibly by an exonuclease activity present in the PCR reaction. The comparison of the amino acid sequence of the cloned fragment compared to the published sequence is shown in Figure 4.

Isolation of pSGLit2tylAII

To add the missing 5'-nucleotides, pSGLit2 was digested with *Pac*I/*Xba*I and the vector fragment was isolated and ligated with the *Pac*I/*Xba*I digested insert fragment of pUC19*tylAII*. The ligated DNA was used to transform *E. coli* ET12567 and plasmid pSGLit2*tylAII* (*dam*$^-$) was isolated.

Isolation of plasmid pUC19eryCVI

The *eryCVI* gene was amplified by PCR using primer BIOSG28 5'-GGGCATATGTACGAGGG CGGGTTCGCCGAGCTTTACGACC-3' (SEQ ID NO: 21) and BIOSG29 5'-GGGGTCTAGAGGTCAT CCGCGCACACCGACGAACAACCCG-3' (SEQ ID NO: 22) and plasmid pNCO62 (Gaisser *et al.*, 1997) as a template. The PCR product was cloned into *Sma*I digested pUC19 using standard techniques and plasmid pUC19*eryCVI* was isolated and verified by sequence analysis.

Isolation of plasmid pSGLit2eryCVI

Plasmid pUC19*eryCVI* was digested with *Nde*I/*Xba*I and ligated with the *Nde*I/*Xba*I digested vector fragment of pSGLit2 followed by transformation of *E. coli* ET12567. Plasmid pSGLit2*eryCVI* (*dam*$^-$) was isolated.

Isolation of plasmid pSG144tylAI

Plasmid pSG144 and pUC19*tylAI* were digested with *Nde*I/*Xba*I and the insert band of pUC19*tylAI* and the vector band of pSG144 were isolated, ligated and used to transform *E. coli* DH10B. Plasmid pSG144*tylAI* was isolated using standard protocols.

Isolation of plasmid pSG144tylAItylAII

Plasmid pSGLit2*tylAII* (*dam*$^-$) was digested with *Xba*I and ligated with *Xba*I digested plasmid pSG144*tylAI*. The ligation was used to transform *E. coli* DH10B and plasmid pSG144*tylAItylAII* was isolated and verified using standard protocols.

Isolation of plasmid pSGLit2tylMIII

Plasmid pUC18tylM3 (Isolation described in WO01/79520) was digested with *Nde*I/*Xba*I and the insert band and the vector band of *Nde*I/*Xba*I digested pSGLit2 were isolated, ligated and used to transform *E. coli* ET12567. Plasmid pSGLit2*tylMIII* (*dam*$^-$) was isolated using standard protocols. The construct was verified using restriction digests and sequence analysis.

Isolation of plasmid pSG144tylAItylAIItylMIII

Plasmid pSGLit2*tylMIII* (*dam*$^-$) was digested with *Xba*I and the insert band was ligated with *Xba*I digested plasmid pSG144*tylAItylAII*. The ligation was used to transform *E. coli* DH10B and plasmid pSG144*tylAItylAIItylMIII* no36 was isolated using standard protocols. The construct was verified using restriction digests and sequence analysis.

Isolation of plasmid pSGLit2tylB

Plasmid pUC18*tylB* (Isolation described in WO01/79520) was digested with *Pac*I/*Xba*I and the insert band and the vector band of *Pac*I/*Xba*I digested pSGLit2 were isolated, ligated and used to transform *E. coli* ET12567. Plasmid pSGLit2*tylB* no1 (*dam*$^-$) was isolated using standard protocols.

Isolation of plasmid pSG144tylAItylAIItylMIIItylB

Plasmid pSGLit2*tylB* (*dam*$^-$) was digested with *Xba*I and the insert band was ligated with *Xba*I digested plasmid pSG144*tylAItylAIItylMIII*. The ligation was used to transform *E. coli* DH10B and plasmid pSG144*tylAItylAIItylMIIItylB* no5 was isolated using standard protocols and verified by restriction digests and sequence analysis.

Isolation of plasmid pUC18tylIa

Primers BIOSG 88 5'-GGG<u>CATATG</u>GCGGCGAGCACTACGACGGAGGGGAATGT-3' (SEQ ID NO: 23) and BIOSG 89 5'-GGG<u>TCTAGA</u>GGTCACGGGTGGCTCCTGCCGGCCCTCAG-3' (SEQ ID NO: 24) were used to amplify *tylIa* using a plasmid carrying the *tyl* region (accession number u08223.em_pro2) comprising ORF1 (cytochrome P450) to the end of ORF2 (TylB) as a template. Plasmid pUC*tylIa* no1 was isolated using standard procedures and the construct was verified using sequence analysis.

Isolation of plasmid pSGLit2tylIa

Plasmid pUC*tylIa* no1 was digested with *Nde*I/*Xba*I and the insert band and the vector band of *Nde*I/*Xba*I digested pSGLit2 were isolated, ligated and used to transform *E. coli* ET12567. Plasmid pSGLit2*tylIa* no 54 (*dam*$^-$) was isolated using standard protocols. The construct was verified using sequence analysis.

Isolation of plasmid pSG144tylAItylAIItylMIIItylBtylIa

Plasmid pSGLit2*tylIa* (*dam*$^-$) was digested with *Xba*I and the insert band was ligated with *Xba*I digested plasmid pSG144*tylAItylAIItylMIIItylB*. The ligation was used to transform *E. coli* DH10B and plasmid pSG144*tylAItylAIItylMIIItylBtylIa* no3 was isolated using standard protocols and verified by restriction digests and sequence analysis.

Isolation of plasmid pSGLit1tylMIeryCIII

Plasmid pUC*tylMI* (Isolation described in WO01/79520) was *Pac*I digested and the insert was ligated with the *Pac*I digested vector fragment of pSGLit1*eryCIII* using standard procedures. Plasmid

pSGLit1*tylMIeryCIII* no20 was isolated and the orientation was confirmed by restriction digests and sequence analysis.

Isolation of gene cassette pSG144tylAItylAIItylMIIItylBtyl1atylMIeryCIII

Plasmid pSGLit1*tylMIeryCIII* no20 was digested with *Xba*I/*Bgl*II and the insert band was isolated and ligated with the *XbaI/Bgl*II digested vector fragment of plasmid pSG144*tylAItylAIItylMIIItylBtylIa* no3. Plasmid *pSG144tylAItylAIItylMIIItylBtyl1atylMIeryCIII* was isolated using standard procedures and the construct was confirmed using restriction digests and sequence analysis. Plasmid preparations were used to transform *S. erythraea* mutant strains with standard procedures.

Isolation of plasmid pSGKC1

To prevent the conversion of the substrate 3-*O*-mycarosyl erythronolide B to 3,5-di-*O*-mycarosyl erythronolide B a further chromosomal mutation was introduced into *S. erythraea* SGQ2 (Isolation described in WO 01/79520) to prevent the biosynthesis of L-mycarose in the strain background. Plasmid pSGKC1 was isolated by cloning the approximately 0.7 kb DNA fragment of the *eryBVI* gene by using PCR amplification with cosmid2 or plasmid pGG1 (WO01/79520) as a template and with the primers 646 5'-CATCGTCAAGGAGTTCGACGGT- 3' (SEQ ID NO: 25) and 874 5'-GCCAGCTCGGCGACGTCC ATC- 3' (SEQ ID NO: 26) using standard protocols. Cosmid 2 containing the right hand site of the *ery*-cluster was isolated from an existing cosmid library (Gaisser *et al.*, 1997) by screening with *eryBV* as a probe using standard techniques. The amplified DNA fragment was isolated and cloned into *Eco*RV digested pKC1132 (Bierman *et al.*, 1992) using standard methods. The ligated DNA was used to transform *E. coli* DH10B and plasmid pSGKC1 was isolated using standard molecular biological techniques. The construct was verified by DNA sequence analysis.

Isolation of S. erythraea Q42/1 (Biot-2166)

Plasmid pSGKC1 was used to transform *S. erythraea* SGQ2 using standard techniques followed by selection with apramycin. Thiostrepton/apramycin resistant transformant *S. erythraea* Q42/1 was isolated.

Bioconversion using S. erythraea Q42/1pSG144tylAItylAIItylMIIItylBtyl1atylMIeryCIII

Bioconversion assays using 3-*O*-mycarosyl erythronolide B are carried out as described in General Methods. Improved levels of mycaminosyl erythromycin A are detected in bioconversion assays using *S. erythraea* Q42/1pSG144*tylAItylAIItylMIIItylBtyl1atylMIeryCIII* compared to bioconversion levels previously observed (WO01/79520).

Example 2: Isolation of mycaminosyl tylactone using gene cassette pSG144*tylAItylAIItylMIIItylBtylIatylMItylMII*

Isolation of plasmid pSGLit1tylMItylMII

Plasmid pUC*tylMI* (Isolation described in WO01/79520) was *Pac*I digested and the insert was ligated with the *Pac*I digested vector fragment of pSGLit1*tylMII* using standard procedures. Plasmid pSGLit1*tylMItylMII* no16 was isolated and the construct was confirmed by restriction digests and sequence analysis.

Isolation of plasmid pSG144tylAItylAIItylMIIItylBtylIatylMItylMII

Plasmid pSGLit1*tylMItylMII* no16 was digested with *Xba*I/*Bgl*II and the insert band was isolated and ligated with the *Xba*I/*Bgl*II digested vector fragment of plasmid pSG144*tylAItylAIItylMIIItylBtylIa* no3. Plasmid pSG144*tylAItylAIItylMIIItylBtyl1atylMItylMII* was isolated using standard procedures and the construct was confirmed using restriction digests and sequence analysis. The plasmid was isolated and used for transformation of *S. erythraea* mutant strains using standard protocols.

Bioconversion using gene cassette pSG144tylAItylAIItylMIIItylBtyl1atylMItylMII

The conversion of fed tylactone to mycaminosyl tylactone was assessed in bioconversion assays using *S. erythraea* Q42/1pSG144*tylAItylAIItylMIIItylBtyl1atylMItylMII*. Bioconversion assays were carried out using standard protocols. The analysis of the culture showed the major ion to be 568.8 $[M+H]^+$ consistent with the presence of mycaminosyl tylactone. Fragmentation of this ion gave a daughter ion of m/z 174, as expected for protonated mycaminose. No tylactone was detected during the analysis of the culture extracts, indicating that the bioconversion of the fed tylactone was complete.

Recently, a homologue of TylIa was identified in the biosynthetic pathway of dTDP-3-acetamido-3,6-dideoxy-alpha-D-galactose in *Aneurinibacillus thermoaerophilus* L420-91^{T*} (Pfoestl *et al.*, 2003) and the function was postulated as a novel type of isomerase capable of synthesizing dTDP-6-deoxy-D-xylohex-3-ulose from dTDP-6-deoxy-D-xylohex-4-ulose.

Example 3: Bioconversion of 3-*O*-mycarosyl erythronolide B to 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycins using gene cassette pSG144*8/27/95/21/44/193/6eryCIII* *(pSG144angAIangAIIorf14angMIIIangBangMIeryCIII)*.

Cloning of angMIII by isolating plasmid Lit1/4

The gene *angMIII* was amplified by PCR using the primers BIOSG61 5'-GGG<u>CATATG</u>AGCCCCGCACCCGCCACCGAGGACCC -3' (SEQ ID NO: 27) and BIOSG62 5'-

GGTCTAGAGGTCAGTTCCGCGGTGCGGTGGCGGGCAGGTCAC -3' (SEQ ID NO: 28). Cosmid5B2 containing a fragment of the angolamycin biosynthetic pathway was used as template. The 1.4 kb PCR fragment (PCR no1) was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid Lit*1/4* was isolated with an *Nde*I site overlapping the start codon of *angMIII* and an *Xba*I site following the stop codon. The construct was verified by sequence analysis.

Isolation of plasmid pSGLit21/4

Plasmid Lit*1/4* was digested with *Nde*I/*Xba*I and the about 1.4 kb fragment was isolated and ligated to *Nde*I/*Xba*I digested DNA of pSGLit2. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit2*1/4* no7 (*dam*⁻) was isolated. This construct was digested with *Xba*I and used for the construction of gene cassettes.

Cloning of angMII by isolating plasmid Lit2/8

The gene *angMII* was amplified by PCR using the primers BIOSG63 5'-GGGCATATGCGTATC CTGCTGACGTCGTTCGCGCACAACAC -3' (SEQ ID NO: 29) and BIOSG64 5'-GGTCTAGAGGTCA GGCGCGGCGGTGCGCGGCGGTGAGGCGTTCG -3' (SEQ ID NO: 30) and cosmid5B2 containing a fragment of the angolamycin biosynthetic pathway was used as template. The 1.3 kb PCR fragment (PCR no2) was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid Lit*2/8* was isolated with an *Nde*I site overlapping the start codon of *angMII* and an *Xba*I site following the stop codon. The construct was verified by sequence analysis.

Cloning of angMII by isolating plasmid pLitangMII(BglII)

The gene *angMII* was amplified by PCR using primers BIOSG63 5'-GGGCATATGCGTATCCT GCTGACGTCGTTCGCGCACAACAC -3' (SEQ ID NO: 29) and BIOSG80 5'-GGAGATCTGGCGCG GCGGTGCGCGGCGGTGAGGCGTTCG -3' (SEQ ID NO: 31) and cosmid5B2 containing a fragment of the angolamycin biosynthetic pathway as template. The 1.3 kb PCR fragment was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid Lit*angMII(BglII)*no8 was isolated with an *Nde*I site overlapping the start codon of *angMII* and a *Bgl*II site instead of a stop codon thus allowing the addition of a *his*-tag. The construct was verified by sequence analysis.

Isolation of plasmid pSG-Lit1angMII

Plasmid Lit*angMII*(*Bgl*II) was digested with *Nde*I/*Bgl*II and ligated with the *Nde*I/*Bgl*II digested vector fragment of pSGLit1. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit1*angMII* (*dam*⁻) was isolated using standard procedures.

Cloning of angMI by isolating plasmid Lit3/6

The gene *angMI* was amplified by PCR using the primers BIOSG65 5'-GGGCATATGAAC CTCGAATACAGCGGCGACATCGCCCGGTTG -3' (SEQ ID NO: 32) and BIOSG66 5'-GGTCTAGAGGTCAGGCCTGGACGCCGACGAAGAGTCCGCGGTCG -3' (SEQ ID NO: 33) and cosmid5B2 containing a fragment of the angolamycin biosynthetic pathway was used as template. The 0.75 kb PCR fragment (PCR no3) was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid Lit*3/6* was isolated with an *Nde*I site overlapping the start codon of *angMI* and an *Xba*I site following the stop codon. The construct was verified by sequence analysis.

Isolation of plasmid pSGlit23/6 no8

Plasmid Lit*3/6* was digested with *Nde*I/*Xba*I and the about 0.8 kb fragment was isolated and ligated to *Nde*I/*Xba*I digested DNA of pSGLit2. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit2*3/6* no8 (*dam*$^-$) was isolated. This construct was digested with *Xba*I and the isolated about 1 kb fragment was used for the assembly of gene cassettes.

Cloning of angB by isolating plasmid Lit4/19

The gene *angB* was amplified by PCR using the primers BIOSG67 5'-GGGCATATGACTACCT ACGTCTGGGACTACCTGGCGG -3' (SEQ ID NO: 34) and BIOSG68 5'-GGTCTAGAGGTCAGAGC GTGGCCAGTACCTCGTGCAGGGC -3' (SEQ ID NO: 35) and cosmid4H2 containing a fragment of the angolamycin biosynthetic pathway was used as template. The 1.2 kb PCR fragment (PCR no4) was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid Lit*4/19* was isolated with an *Nde*I site overlapping the start codon of *angB* and an *Xba*I site following the stop codon. The construct was verified by sequence analysis.

Isolation of plasmid pSGlit24/19

Plasmid Lit*4/19* was digested with *Nde*I/*Xba*I and the 1.2 kb fragment was isolated and ligated into *Nde*I/*Xba*I digested DNA of pSGLit2. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit2*4/19* no24 (*dam*$^-$) was isolated. This construct was digested with *Xba*I and the isolated 1.2 kb fragment was used for the assembly of gene cassettes.

Cloning of orf14 by isolating plasmid Lit5/2

The gene *orf14* was amplified by PCR using the primers BIOSG69 5'-GGGCATATGGTGAA CGATCCGATGCCGCGCGGCAGTGGCAG-3' (SEQ ID NO: 36) and BIOSG70 5'-GGTCTAGAGGT CAACCTCCAGAGTGTTTCGATGGGGTGGTGGG-3' (SEQ ID NO: 37) and cosmid4H2 containing a fragment of the angolamycin biosynthetic pathway was used as template. The 1.0 kb PCR fragment (PCR

no5) was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid Lit*5/2* was isolated with an *Nde*I site overlapping the start codon of *ORF14* and an *Xba*I site following the stop codon. The construct was verified by sequence analysis.

Isolation of plasmid pSGlit25/2 no24

Plasmid Lit*5/2* was digested with *Nde*I/*Xba*I and the approximately 1 kb fragment was isolated and ligated to *Nde*I/*Xba*I digested DNA of pSG*Lit2*. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit2*5/2* no24 (*dam*$^-$) was isolated. This construct was digested with *Xba*I, the about 1 kb fragment isolated and used for the assembly of gene cassettes.

Isolation of plasmid pSGlit27/9 no15

Plasmid Lit*7/9* was digested with *Nde*I/*Xba*I and the approximately 1 kb fragment was isolated and ligated to *Nde*I/*Xba*I digested DNA of pSGLit2. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit2*7/9* no15 (*dam*$^-$) was isolated. This construct was digested with *Xba*I and the isolated 1 kb fragment was used for the assembly of gene cassettes.

Cloning of angAI (orf2) by isolating plasmid Lit8/2

The gene *angAI* was amplified by PCR using the primers BIOSG73 5'-GGGCATATGAAGGGC ATCATCCTGGCGGGCGGCAGCGGC-3' (SEQ ID NO: 38) and BIOSG74 5'-GGTCTAGAGGTCAT GCGGCCGGTCCGGACATGAGGGTCTCCGCCAC-3' (SEQ ID NO: 39) and cosmid4H2 containing a fragment of the angolamycin biosynthetic pathway was used as template. The around 1.0 kb PCR fragment (PCR no8) was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid Lit*8/2* was isolated with an *Nde*I site overlapping the start codon of *angAI* and an *Xba*I site following the stop codon. The construct was verified by sequence analysis.

Cloning of angAII (orf3) by isolating plasmid Lit7/9

The gene *angAII* was amplified by PCR using the primers BIOSG71 5'-GGGCATATGCGGCTG CTGGTCACCGGAGGTGCGGGC-3' (SEQ ID NO: 40) and BIOSG72 5'-GGTCTAGAGGTCAGTCG GTGCGCCGGGCCTCCTGCG-3' (SEQ ID NO: 41) and cosmid4H2 containing a fragment of the angolamycin biosynthetic pathway was used as template. The 1.0 kb PCR fragment was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid Lit*7/9* was isolated with an *Nde*I site overlapping the start codon of *angAII* and an *Xba*I site following the stop codon. The construct was verified by sequence analysis.

Isolation of plasmid pSGlit28/2 no18 (pSGLit2angAI)

Plasmid Lit*8/2* was digested with *Nde*I/*Xba*I and the 1 kb fragment was isolated and ligated to *Nde*I/*Xba*I digested DNA of pSGLit2. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit2*8/2* no18 (*dam*$^-$) was isolated.

Isolation of plasmid pSG1448/2 (pSG144angAI)

Plasmid Lit*8/2* was digested with *Nde*I/*Xba*I and the approximately 1 kb fragment was isolated and ligated with *Nde*I/*Xba*I digested DNA of pSG144. The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/2* (*dam*$^-$) (pSG144*angAI*) was isolated using standard procedures. This construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/9 (pSG144angAIangAII)

Plasmid pSGLit2*7/9* (isolated from *E.coli* ET12567) was digested with *Xba*I and the 1 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/2* (pSG144*angAI*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/9* (pSG144*angAIangAII*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/91/4 (pSG144angAIangAIIangMIII)

Plasmid pSGLit2*1/4* (isolated from *E. coli* ET12567) was digested with *Xba*I and the 1.4 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/9* (pSG144*angAIangAII*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4* (pSG144*angAIangAIIangMIII*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/91/44/19 (pSG144angAIangAIIangMIIIangB)

Plasmid pSGLit2*4/19* (isolated from *E. coli* ET12567) was digested with *Xba*I and the about 1.2 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/91/4* (pSG144*angAIangAIIangMIII*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/44/19* (pSG144*angAIangAIIangMIIIangB*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/91/44/193/6 (pSG144angAIangAIIangMIIIangBangMI)

Plasmid pSGLit23/6 (isolated from *E. coli* ET12567) was digested with *Xba*I and the about 0.8 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/91/44/19* (pSG144*angAIangAIIangMIIIangB*). The ligation was used to transform *E. coli* DH10B and plasmid

pSG1448/27/91/44/193/6 (pSG144*angAIangAIIangMIIIangBangMI*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/91/44/193/6eryCIII (pSG144angAIangAIIangMIIIangBangMIeryCIII)

Plasmid pSGLit1*eryCIII* (isolated from *E. coli* ET12567) was digested with *Xba*I/*Bgl*II and the about 1.2 kb fragment was isolated and ligated with the *Xba*I digested and partially *Bgl*II digested vector fragment of pSG1448/27/91/44/193/6 (pSG144*angAIangAIIangMIIIangBangMI*). The *Bgl*II partial digest was necessary due to the presence of a *Bgl*II site in *angB*. The ligation was used to transform *E. coli* DH10B and plasmid pSG1448/27/91/44/193/6*eryCIII* no9 (pSG144*angAIangAIIangMIIIangBangMIeryCIII*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis. EryCIII carries a *his*-tag fusion at the end.

*Bioconversion of 3-O-mycarosyl erythronolide B to 5-O-dedesosaminyl-5-O-mycaminosyl erythromycin A using S. erythraea Q42/1*pSG1448/27/91/44/193/6*eryCIII* no9 (pSG144*angAIangAIIangMIIIangBangMIeryCIII*)

The *S. erythraea* strain Q42/1pSG1448/27/91/44/193/6*eryCIII* was grown and bioconversions with fed 3-*O*-mycarosyl erythronolide B were performed as described in the General Methods. The cultures were analysed and a small amount of a compound with m/z 750 was detected consistent with the presence of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A.

Isolation of plasmid pSG1448/27/95/2 (pSG144angAIangAIIorf14)

Plasmid pSGLit25/2 (isolated from *E. coli* ET12567) was digested with *Xba*I and the about 1 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG1448/27/9 (pSG144*angAIangAII*). The ligation was used to transform *E. coli* DH10B and plasmid pSG1448/27/95/2 (pSG144*angAIangAIIorf14*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/95/21/4 (pSG144angAIangAIIorf14angMIII)

Plasmid pSGLit21/4 (isolated from *E. coli* ET12567) was digested with *Xba*I and the 1.4 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG1448/27/95/2 (pSG144*angAIangAIIorf14*). The ligation was used to transform *E. coli* DH10B and plasmid pSG1448/27/95/21/4 (pSG144*angAIangAIIorf14angMIII*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/95/21/44/19 (pSG144angAIangAIIorf14angMIIIangB)

Plasmid pSGLit2*4/19* (isolated from *E. coli* ET12567) was digested with *Xba*I and the 1.2 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/95/21/4* (pSG144*angAIangAIIorf14angMIII*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/95/21/44/19* (pSG144*angAIangAIIorf14angMIIIangB*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/95/21/44/193/6eryCIII (pSG144angAIangAIIorf14angMIIIangBangMIeryCIII)

Plasmid pSG144*8/27/91/44/193/6eryCIII* no9 was digested with *Bgl*II and the about 2 kb fragment was isolated and ligated with the *Bgl*II digested vector fragment of pSG144*8/27/95/21/44/19* (pSG144*angAIangAIIorf14angMIIIangB*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/95/21/44/193/6eryCIII* (pSG144*angAIangAIIorf14angMIIIangBangMIeryCIII*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis. EryCIII carries a *his*-tag fusion at the end. The construct was used to transform *S. erythraea* SGQ2 using standard procedures.

Bioconversion of 3-O-mycarosyl erythronolide B to 5-O-dedesosaminyl-5-O-mycaminosyl erythromycin A

The *S. erythraea* strain SGQ2pSG144*8/27/95/21/44/193/6eryCIII* was grown and bioconversions with fed 3-*O*-mycarosyl erythronolide B were performed as described in the General Methods. The cultures were analysed and improved amounts of a compound with m/z 750 was detected consistent with the presence of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A. Similar results were obtained with the *S. erythraea* strain Q42/1 containing the gene cassette pSG144*8/27/95/21/44/193/6eryCIII*. 16 mg of the compound with m/z 750 was purified and the structure of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A was confirmed by NMR analysis (See Table I and Figure 1).

Table II: ^{1}H and ^{13}C NMR data for 5-O-dedesosaminyl-5-O-mycaminosyl erythromycin A (BC156)

Position	δ_H	Multiplicity	Coupling	δ_C
1				175.4
2	2.83	dq	9.6, 7.1	44.9
3	3.91	dd	9.7, 1.6	80.0
4	2.00	m		39.1
5	3.53	d	6.8	85.4
6				74.8
7	1.66	dd	14.8, 2.2	38.5
	1.82	dd	14.8, 11.4	
8	2.69	dqd	11.3, 7.0, 2.2	44.9
9				221.6
10	3.06	qd	6.9, 1.3	38.0
11	3.81	d	1.3	68.9

Position	δ_H	Multiplicity	Coupling	δ_C
12				74.6
13	5.04	dd	11.0, 2.3	76.8[a]
14	1.47	dqd	14.3, 11.0, 7.2	21.1
	1.91	ddq	14.3, 7.5, 2.2	
15	0.83	dd	7.4, 7.4	10.6
16	1.18	d	7.1	16.0
17	1.03	d	7.4	9.7
18	1.44	s		26.6
19	1.16	d	7.0	18.3
20	1.14	d	7.0	12.0
21	1.12	s		16.2
1′	4.87	d	4.8	96.4
2′	1.55	dd	15.2, 4.8	34.9
	2.32	dd	15.2, 0.9	
3′				72.8
4′	3.01	d	9.3	77.8
5′	3.99	dq	9.3, 6.2	65.6
6′	1.27	d	6.2	18.5
7′	1.23	s		21.4
8′	3.29	s		49.4
1′′	4.43	d	7.4	103.3
2′′	3.56	dd	10.5, 7.3	71.3
3′′	2.48	dd	10.3, 10.3	70.6
4′′	3.09	dd	9.9, 9.0	70.2
5′′	3.31	dq	9.0, 6.1	72.9
6′′	1.29	d	6.1	18.1
7′′	2.58	s		41.7

[a] This carbon was assigned from the HMQC spectrum

Example 4: Isolation of mycaminosyl tylactone

Isolation of plasmid pSG1448/27/95/21/44/193/6tylMII (pSG144angAIangAIIorf14angMIIIangB3/6tylMII)

Plasmid pSG1448/27/91/44/193/6tylMII no9 was digested with *Bgl*II and the about 2 kb fragment was isolated and ligated with the *Bgl*II digested vector fragment of pSG1448/27/95/21/44/19 (pSG144*angAIangAIIorf14angMIIIangB*). The ligation was used to transform *E. coli* DH10B and plasmid pSG1448/27/95/21/44/193/6tylMII (pSG144*angAIangAIIorf14angMIIIangBangMItylMII*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis. TylMII carries a *his*-tag fusion at the end.

Bioconversion of tylactone to mycaminosyl tylactone

The *S. erythraea* strain Q42/1pSG1448/27/95/21/44/193/6tylMII is grown and bioconversions with fed tylactone is performed as described in the General Methods. The cultures are analysed and a compound with m/z 568 is detected consistent with the presence of mycaminosyl tylactone.

Example 5: Isolation of 5-*O*-dedesosaminyl-5-*O*-angolosaminyl erythromycins using gene cassette pSG144*8/27/91/4spnO5/2p4/193/6tylMII* by bioconversion of 3-*O*-mycarosyl erythronolide B.

Isolation of plasmid conv no1

For the multiple use of promoter sequences in *act*-controlled gene cassettes a 240 bp fragment was amplified by PCR using the primers BIOSG78 5'-GGGCATATGTGTCCTCCTTAATTAATCGAT GCGTTCGTCC-3' (SEQ ID NO: 42) and BIOSG79 5'-GGAGATCTGGTCTAGATCGTGTTCCCCTCC CTGCCTCGTGGTCCCTCACGC -3' (SEQ ID NO: 43) and plasmid pSG142 (Gaisser *et al.*, 2000) as template. The 0.2 kb PCR fragment (PCR no5) was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid conv no1 was isolated. The construct was verified by sequence analysis.

Isolation of pSGLit3relig1

Plasmid conv no1 was digested with *Nde*I/*Bgl*II and the about 0.2 kb fragment was isolated and ligated with the *Bam*HI/*Nde*I digested vector fragment of pSGLit2. The ligation was used to transform *E. coli* DH10B and plasmid pSGLit3relig1 was isolated using standard procedures. This construct was verified using restriction digests and sequence analysis.

Isolation of plasmid pSGlit34/19

Plasmid Lit*4/19* was digested with *Nde*I/*Xba*I and the 1.2 kb fragment was isolated and ligated to *Nde*I/*Xba*I digested DNA of pSGLit3. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit3*4/19* no23 was isolated. This construct was digested with *Xba*I and the isolated 1.4 kb fragment was used for the assembly of gene cassettes.

Cloning of orf4 by isolating plasmid Lit6/4

The gene *orf4* was amplified by PCR using the primers BIOSG75 5'-GGGCATATGAGCACCC CTTCCGCACCACCCGTTCCG-3' (SEQ ID NO: 44) and BIOSG76 5'-GGTCTAGAGGTCAGTACAG CGTGTGGGCACACGCCACCAG-3' (SEQ ID NO: 45) and cosmid4H2 containing a fragment of the angolamycin biosynthetic pathway was used as template. The 2.5 kb PCR fragment (PCR no6) was cloned using standard procedures and *Eco*RV digested plasmid Litmus28. Plasmid Lit*6/4* was isolated with an *Nde*I site overlapping the start codon of *orf4* and an *Xba*I site following the stop codon. The construct was verified by sequence analysis.

Isolation of plasmid pSGlit26/4 no9

Plasmid Lit*6/4* was digested with *Nde*I/*Xba*I and the DNA was isolated and ligated to *Nde*I/*Xba*I digested DNA of pSGLit2. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit2*6/4* no9 was isolated. This construct was confirmed by restriction digests and sequence analysis.

Cloning of spnO by isolating plasmid pUC19spnO

The gene *spnO* from the spinosyn biosynthetic gene cluster of *Saccharopolyspora spinosa* was amplified by PCR using the primers BIOSG41 5'-GGGCATATGAGCAGTTCTGTCGAAGCTGAGGC AAGTG-3' (SEQ ID NO: 46) and BIOSG42 5'-GGTCTAGAGGTCATCGCCCCAACGCCCACAAGCT ATGCA GG-3' (SEQ ID NO: 47) and genomic DNA of *S. spinosa* as template. The about 1.5 kb PCR fragment was cloned using standard procedures and *Sma*I digested plasmid pUC19. Plasmid pUC19*spnO* no2 was isolated with an *Nde*I site overlapping the start codon of *spnO* and an *Xba*I site following the stop codon. The construct was verified by sequence analysis.

Isolation of plasmid pSGlit2spnO no4

Plasmid pUC19*spnO* was digested with *Nde*I/*Xba*I and the 1.5 kb fragment was isolated and ligated to *Nde*I/*Xba*I digested DNA of pSGLit2. The ligation was used to transform *E. coli* ET12567 and plasmid pSGLit2*spnO* no 4 was isolated using standard procedures. This construct was digested with *Xba*I and the isolated 1.5 kb fragment was used for the assembly of gene cassettes.

Isolation of plasmid pSG1448/27/91/4spnO (pSG144angAIangAIIangMIIIspnO)

Plasmid pSGLit2*spnO* no4 (isolated from *E. coli* ET12567) was digested with *Xba*I and the 1.5 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/91/4* (pSG144*angAIangAIIangMIII*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4spnO* (pSG144*angAIangAIIangMIIIspnO*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/91/4spnO5/2 (pSG144angAIangAIIangMIIIspnOangorf14)

Plasmid pSGLit2*5/2* no24 (isolated from *E. coli* ET12567) was digested with *Xba*I and the 1 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/91/4spnO* (pSG144*angAIangAIIangMIIIspnO*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4spnO5/2* (pSG144*angAIangAIIangMIIIspnOangorf14*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/91/4spnO5/2p4/19 (pSG144angAIangAIIangMIIIspnOangorf14pangB)

Plasmid pSGLit3*4/19* no23 (isolated from *E. coli* ET12567) was digested with *Xba*I and the about 1.4 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/91/4spnO5/2* (pSG144*angAIangAIIangMIIIspnOangorf14*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4spnO5/2p4/19* (pSG144*angAIangAIIangMIIIspnOangorf14pangB*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis. 'p' indicates the presence of the promoter region in front of *angB* to emphasize the presence of multiple promoter sites in the construct.

Isolation of plasmid pSG1448/27/91/4spnO5/2p4/193/6eryCIII (pSG144angAIangAIIangMIIIspnOorf14pangBangMIeryCIII)

Plasmid pSG144*8/27/91/44/193/6eryCIII* no9 was digested with *Bgl*II and the about 2 kb fragment was isolated and ligated with the *Bgl*II digested vector fragment of pSG144*8/27/91/4spnO5/2p4/19* (pSG144*angAIangAIIangMIIIspnOorf14pangB)*. The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4spnO5/2p4/193/6eryCIII* (pSG144*angAIangAIIangMIIIspnOorf14pangBangMIeryCIII*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis. EryCIII carries a *his*-tag fusion at the end. 'p' indicates the presence of the promoter region in front of *angB* to emphasize the presence of multiple promoter sites in the construct. The plasmid construct was used to transform mutant strains of *S. erythraea* using standard procedures.

Bioconversion of 3-O-mycarosyl erythronolide B to 5-O-dedesosaminyl-5-O-angolosaminyl erythromycins

Strain *S. erythraea* Q42/1pSG144*8/27/91/4spnO5/2p4/193/6eryCIII* was grown and bioconversions with fed 3-*O*-mycarosyl erythronolide B were performed as described in the General Methods. The cultures were analysed and peaks with m/z 704, m/z 718 and m/z 734 consistent with the presence of angolosaminyl erythromycin D, B and A, respectively, were observed.

Example 6: Production of 5-*O*-angolosaminyl tylactone

Isolation of plasmid pSG1448/27/91/4spnO5/2p4/193/6tylMII (pSG144angAIangAIIangMIIIspnOorf14pangBangMItylMII)

Plasmid pSG1448/27/91/44/193/6*tylMII* no9 was digested with *Bgl*II and the about 2 kb fragment was isolated and ligated with the *Bgl*II digested vector fragment of pSG144*8/27/91/4spnO5/2p4/19* (pSG144*angAIangAIIangMIIIspnOorf14pangB)*. The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4spnO5/2p4/193/6tylMII* *(pSG144angAIangAIIangMIIIspnOorf14pangBangMItylMII)* was isolated using standard protocols. The

construct was verified with restriction digests and sequence analysis. TylMII carries a *his*-tag fusion at the end. The plasmid was used to transform mutant strains of *S. erythraea* applying standard protocols. 'p' indicates the presence of the promoter region in front of *angB* to emphasize the presence of multiple promoter sites in the construct.

Isolation of S. erythraea 18A1(BIOT-2634)

To introduce a deletion comprising the PKS and majority of post PKS genes in *S. erythraea* a region of the left hand side of the *ery-* cluster (LHS) containing a portion of *eryCI*, the complete *ermE* gene and a fragment of the *eryBI* gene were cloned together with a region of the right hand side of the *ery-* cluster (RHS) containing a portion of the *eryBVII* gene, the complete *eryK* gene and a fragment of DNA adjacent to *eryK*. This construct should enable homologous recombination into the genome in both LHS and RHS regions resulting in the isolation of a strain containing a deletion between these two regions of DNA. The LHS fragment (2201 bp) was PCR amplified using *S. erythraea* chromosomal DNA as template and primers BIdelNde (5'-CC<u>CATATG</u>ACCGGAGTTCGAGGTACGCGGCTTG-3', SEQ ID NO: 48) and BIdelSpe (5'-GAT<u>ACTAGT</u>CCGCCGACCGCACGTCGCTGAGCC-3', SEQ ID NO: 49). Primer BIdelNde contains an *Nde*I restriction site (underlined) and primer BIdelSpe contains a *Spe*I restriction site used for subsequent cloning steps. The PCR product was cloned into the *Sma*I restriction site of pUC19, and plasmid pLSB177 was isolated using standard procedures. The construct was confirmed by sequence analysis. Similarly, RHS (2158 bp) was amplified by PCR using *S. erythraea* chromosomal DNA as template and primers BVIIdelSpe (5'-TGC<u>ACTAGT</u>GGCCGGGCGCTCGACGT CATCGTCGACAT-3', SEQ ID NO: 50) and BVIIdelEco (5'-TC<u>GATATC</u>GTGTCCTGCGGTTTCACC TGCAACGCTG-3', SEQ ID NO: 51). Primer BVIIdelSpe contains a *Spe*I restriction site and primer BVIIdelEco contains an *Eco*RV restriction site. The PCR product was cloned into the *Sma*I restriction site of pUC19 in the orientation with *Spe*I positioned adjacent to *Kpn*I and *Eco*RV positioned adjacent to *Xba*I. The plasmid pLSB178 was isolated and confirmed using sequence analysis. Plasmid pLSB177 was digested with *Nde*I and *Spe*I, the ~2.2kb fragment was isolated and similarly plasmid pLSB178 was digested with *Nde*I and *Spe*I and the ~4.6 kb fragment was isolated using standard methods. Both fragments were ligated and plasmid pLSB188 containing LHS and RHS combined together at a *Spe*I site in pUC19 was isolated using standard protocols. An *Nde*I/*Xba*I fragment (~4.4 kbp) from pLSB188 was isolated and ligated with *Spe*I and *Nde*I treated pCJR24. The ligation was used to transform *E. coli* DH10B and plasmid pLSB189 was isolated using standard methods. Plasmid pLSB189 was used to transform *S. erythraea* P2338 and transformants were selected using thiostrepton. *S. erythraea* Del18 was isolated and inoculated into 6 ml TSB medium and grown for 2 days. A 5% inoculum was used to subculture this strain 3 times. 100 µl of the final culture were used to plate onto R2T20 agar followed by incubation at 30°C to allow sporulation. Spores were harvested, filtered, diluted and plated onto R2T20

agar using standard procedures. Colonies were replica plated onto R2T20 plates with and without addition of thiostrepton. Colonies that could no longer grow on thiostrepton were selected and further grown in TSB medium. *S. erythraea* 18A1 was isolated and confirmed using PCR and Southern blot analysis. The strain was designated LB-1 /BIOT-2634. For further analysis, the production of erythromycin was assessed as described in General Methods and the lack of erythromycin production was confirmed. In bioconversion assays this strain did not further process fed erythronolide B and erythromycin D was hydroxylated at C12 to give erythromycin C as expected, indicating that EryK was still functional.

Bioconversion of tylactone to5-O- angolosaminyl tylactone

Strain *S. erythraea* SGQ2pSG1448*/27/91/4spnO5/2p4/193/6tylMII* was grown and bioconversions with fed tylactone were performed as described in the General Methods. The cultures were extracted and analysed. A compound consistent with the presence of angolosaminyl tylactone was detected. 20 mg of this compound were purified and the structure was confirmed by NMR analysis. A compound consistent with the presence of angolosaminyl tylactone was also obtained when the gene cassette pSG1448*/27/91/4spnO5/2p4/193/6tylMII* was expressed in the *S. erythraea* strain Q42/1 or *S. erythraea* 18A1.

Table III: NMR data for 5-O- βD angolosaminyl Tylactone

#	δ_c	δ_H (mult., Hz)	COSY H-H	HMBC H-C
1	174.4			
2	39.8	1.91 d (16.8)	2b	1, 3
		2.46 dd(16.8, 10.5)	2a, 3	1
3	66.9	3.68 dd (10.5, 1.2)	2b	1
4	40.4	1.56 m	5, 18	3
5	80.7	3.76 d (10.3)	4	4, 7, 18, 19, 1'
6	38.7	2.68 m	7b	
7	33.6	1.45 m		
		1.55 m	6	
8	45.0	2.70 m	21	
9	203.9			
10	118.3	6.26 d (15.5)	11	12
11	147.7	7.27 d (15.5)	10	9, 12, 13, 22
12	133.5			
13	145.4	5.60 d (10.4)	14, 22	11, 14, 22, 23
14	38.3	2.70 m	13, 15, 23	12, 13, 15, 23
15	78.8	4.68 td (9.7, 2.4)	14, 16b	1, 17
16	24.7	1.55 m	15, 16b, 17	15
		1.82 ddd	16a, 17	18

#	δ_c	δ_H (mult., Hz)	COSY H-H	HMBC H-C
17	9.6	0.91 t (7.2)	16	15, 16
18	9.7	0.91 d (7.2)	4	3, 4, 5
19	21.0	1.55 m	20	
20	11.8	0.83 t (7.2)	19	6, 19
21	17.1	1.15 d (6.8)	8	7, 9
22	13.0	1.76 s	13	11, 12, 13
23	16.1	1.05 d (6.5)	14	13, 14, 15
1'	101.0	4.41 d (8.6)	2'	2'
2'	28.0	1.48 m	1', 2b', 3'	1', 3', 4'
		2.05 ddd (10.4, 3.9, 1.6)	2a', 3'	1', 3'
3'	65.8	2.89 td (10.0, 3.9)	2a', 2b', 4'	4'
4'	70.5	3.16 dd (9.5, 9.0)	3', 5'	3', 5', 6'
5'	73.2	3.26 dq (9.6, 6.0)	4', 6'	
6'	17.7	1.3 d (6.0)	5'	

Isolation of plasmid pSG1448/27/91/4spnOp5/2 (pSG144angAIangAIIangMIIIspnOpangorf14)

Plasmid pSGLit3*5/2* (isolated from *E. coli* ET12567) was digested with *Xba*I and the insert fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/91/4spnO* (pSG144*angAIangAIIangMIIIspnO*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4spnOp5/2* (pSG144*angAIangAIIangMIIIspnOpangorf14*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/91/4spnOp5/24/19 (pSG144angAIangAIIangMIIIspnOpangorf14angB)

Plasmid pSGLit2*4/19* (isolated from *E. coli* ET12567) was digested with *Xba*I and the insert fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/91/4spnOp5/2* (pSG144*angAIangAIIangMIIIspnOpangorf14*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4spnOp5/24/19* (pSG144*angAIangAIIangMIIIspnOpangorf14angB*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/91/4spnOp5/24/193/6 (pSG144angAIangAIIangMIIIspnOpangorf14angBangMI)

Plasmid pSGLit2*3/6* (isolated from *E. coli* ET12567) was digested with *Xba*I and the insert fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/91/4spnOp5/24/19* (pSG144*angAIangAIIangMIIIspnOpangorf14angB*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4spnOp5/24/193/6* (pSG144*angAIangAIIangMIIIspnOpangorf14angBangMI*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/91/4spnOp5/24/193/6angMII (pSG144angAIangAIIangMIIIspnOpangorf14angBangMIangMII)

Plasmid pSGLit1*angMII* (isolated from *E. coli* ET12567) was digested with *Xba*I/*Bgl*II and the insert fragment was isolated and ligated with the *Xba*I and partial *Bgl*II digested vector fragment of pSG144*8/27/91/4spnOp5/24/193/6* (pSG144*angAIangAIIangMIIIspnOpangorf14angBangMI*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/91/4spnOp5/24/193/6angMII* (pSG144*angAIangAIIangMIIIspnOpangorf14angBangMIangMII*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis. The plasmid was used to transform mutant strains of *S. erythraea* with standard procedures.

Biotransformation using S. erythraea Q42/1 pSG1448/27/91/4spnOp5/24/193/6angMII (pSG144angAIangAIIangMIIIspnOpangorf14angBangMIangMII)

Biotransformation experiments feeding tylactone are carried out as described in General Methods and the cultures are analysed. Angolosaminyl tylactone is detected.

Isolation of plasmid pSG1448/27/96/4 (pSG144angAIangAIIangorf4)

Plasmid pSG1448/27/9 (pSG144*angAIangAII*) was digested with *Xba*I and treated with alkaline phosphatase using standard protocols. The vector fragment was used for ligations with *Xba*I treated plasmid pSGLit2*6/4* no9 followed by transformations of *E. coli* DH10B using standard protocols. Plasmid pSG144*8/27/96/4* (pSG144*angAIangAIIangorf4*) was isolated using standard procedures and the construct was confirmed by restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/96/4p5/2 (pSG144angAIangAIIangorf4pangorf14)

Plasmid pSGLit3*5/2* (isolated from *E. coli* ET12567) was digested with *Xba*I and the insert fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/96/4* (pSG144*angAIangAIIangorf4*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/96/4p5/2* (pSG144*angAIangAIIangorf4pangorf14*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/96/4p5/21/4 (pSG144angAIangAIIangorf4pangorf14angMIII)

Plasmid pSGLit2*1/4* (isolated from *E. coli* ET12567) was digested with *Xba*I and the 1.4 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/96/4p5/2* (pSG144*angAIangAIIangorf4pangorf14*). The ligation was used to transform *E. coli* DH10B and plasmid

pSG1448/27/96/4p5/21/4 (pSG144*angAIangAIIangorf4pangorf14angMIII*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/96/4p5/21/44/19 (pSG144angAIangAIIangorf4pangorf14angMIIIangB)

Plasmid pSGLit2*4/19* (isolated from *E. coli* ET12567) was digested with *Xba*I and the 1.4 kb fragment was isolated and ligated with the *Xba*I digested vector fragment of pSG144*8/27/96/4p5/21/4* (pSG144*angAIangAIIangorf4pangorf14angMIII*). The ligation was used to transform *E. coli* DH10B and plasmid pSG144*8/27/96/4p5/21/44/19* (pSG144*angAIangAIIangorf4pangorf14angMIIIangB*) was isolated using standard protocols. The construct was verified with restriction digests and sequence analysis.

Isolation of plasmid pSG1448/27/96/4p5/21/44/193/6angMII (pSG144angAIangAIIangorf4pangorf14angMIIIangBangMIangMII)

Plasmid pSG144*8/27/91/4spnOp5/24/193/6angMII* was digested with *Bgl*II and the about 2.2 kb fragment was isolated and used to ligate with the *Bgl*II treated vector fragment of pSG144*8/27/96/4p5/21/44/19*. The ligation was used to transform *E. coli* DH10B using standard procedures and plasmid pSG144*8/27/96/4p5/21/44/193/6angMII* (pSG144*angAIangAIIangorf4pangorf14angMIIIangBangMIangMII)* was isolated. The construct was verified using restriction digests and sequence analysis. The plasmid was used to transform mutant strains of *S. erythraea* with standard protocols.

Bioconversion of tylactone with S. erythraea Q42/1 pSG1448/27/96/4p5/21/44/193/6angMII (pSG144angAIangAIIangorf4pangorf14angMIIIangBangMIangMII)

Biotransformation experiments feeding tylactone are carried out as described in General Methods and the cultures are analysed. Angolosaminyl tylactone is detected.

Example 7: Cloning of *eryK* into the gene cassette pSG144

Isolation of plasmid pUC19eryK

To amplify *eryK* primers eryK1 5'-GG<u>TCTAGA</u>CTACGCCGACTGCCTCGGCGAGGAGCCC-3' (SEQ ID NO: 52) and eryK2: 5'-GG<u>CATATG</u>TTCGCCGACGTGGAAACGACCTGCTGCG-3' (SEQ ID NO: 53) were used and the PCR product was cloned as described for pUC19*eryCVI*. Plasmid pUC19*eryK* was isolated.

Isolation of plasmid pLSB111 (pCJR24eryK)

Plasmid pUC19*eryK* was digested with *Nde*I/*Xba*I and the insert band was ligated with *Nde*I/*Xba*I digested pCJR24. Plasmid pLSB111 (pCJR24*eryK*) was isolated and the construct was verified with restriction digests.

Isolation of plasmid pLSB115

Plasmid pLSB111 (pCJR24*eryK*) was digested with *Nde*I/*Xba*I and the insert fragment was isolated and ligated with the *Nde*I/*Xba*I digested vector fragment of plasmid pSGLit2 and plasmid pLSB115 was isolated using standard protocols. The plasmid was verified using restriction digestion and DNA sequence analysis.

Isolation of plasmid pSG1448/27/95/21/4eryK

Plasmid pLSB115 from *E. coli* ET12567 was digested with *Xba*I and the insert fragment was isolated and ligated with the *Xba*I treated vector fragment of pSG144*8/27/95/21/4* (pSG144*angAIangAIIangorf14angMIII*). The ligation was used to transform *E. coli* DH10B with standard procedures and plasmid pSG144*8/27/95/21/4eryK* (pSG144*angAIangAIIangorf14angMIIIeryK*) is isolated. The construct is confirmed with restriction digests.

Isolation of plasmid pSG1448/27/95/21/4eryK4/19

Plasmid pSGLit24/19 from *E. coli* ET12567 is digested with *Xba*I and the insert fragment is isolated and ligated with the *Xba*I treated vector fragment of plasmid pSG144*8/27/95/21/4eryK*. The ligation is used to transform *E. coli* DH10B with standard procedures and plasmid pSG144*8/27/95/21/4eryK4/19* (pSG144*angAIangAIIangorf14angMIIIeryKangB*) is isolated. The construct is confirmed with restriction digests.

Isolation of plasmid pSG1448/27/95/21/4eryK4/193/6eryCIII

Plasmid pSG144*8/27/95/21/44/193/6eryCIII* is digested with *Bgl*II and the about 2.1 kb fragment is isolated and ligated with the *Bgl*II treated vector fragment of pSG144*8/27/95/21/4eryK4/19*. Plasmid *pSG1448/27/95/21/4eryK4/193/6eryCIII* is isolated using standard procedures and the construct is confirmed using restriction digests. The plasmid is used to transform mutant strains of *S. erythraea* with standard methods.

Bioconversion of 3-O-mycarosyl erythronolide B to 5-O-dedesosaminyl-5-O-mycaminosyl erythromycin A

The *S. erythraea* strain Q42/1pSG144*8/27/95/21/4eryK4/193/6eryCIII* is grown and bioconversions with fed 3-*O*-mycarosyl erythronolide B are performed as described in the General

Methods. The cultures are analysed and a compound with m/z 750 is detected consistent with the presence of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A.

Example 8: Production of 13-desethyl-13-methyl-5-*O*-mycaminosyl erythromycins A and B; 13-desethyl-13-isopropyl-5-*O*-mycaminosyl erythromycin A and B; 13-desethyl-13-secbutyl-5-*O*-mycaminosyl erythromycin A and B

Production of 13-desethyl-13-methyl-3-O-mycarosyl erythronolide B, 13-desethyl-13-isopropyl-3-O-mycarosyl erythronolide B and 13-desethyl-13-secbutyl-3-O-mycarosyl erythronolide B

Plasmid pLS025, (WO 03/033699) a pCJR24-based plasmid containing the DEBS1, DEBS2 and DEBS3 genes, in which the loading module of DEBS1 has been replaced by the loading module of the avermectin biosynthetic cluster, was used to transform *S. erythraea* JC2ΔeryCIII (isolated using techniques and plasmids described previously (Rowe *et al.*, 1998; Gaisser *et al.*, 2000)) using standard techniques. The transformant JC2ΔeryCIIIpLS025 was isolated and cultures were grown using standard protocols. Cultures of *S. erythraea* JC2ΔeryCIIIpLS025 are extracted using methods described in the General Methods section and the presence of 3-*O*-mycarosyl erythronolide B, 13-desethyl-13-methyl-3-*O*-mycarosyl erythronolide B, 13-desethyl-13-isopropyl-3-*O*-mycarosyl erythronolide B and 13-desethyl-13-secbutyl-3-*O*-mycarosyl erythronolide B in the crude extract is verified by LCMS analysis.

Production of 13-desethyl-13-methyl-5-O-dedesosminyl-5-O-mycaminosyl erythromycin A and B, 13-desethyl-13-isopropyl-5-O-dedesosaminyl-5-O-mycaminosyl erythromycin A and B, 13-desethyl-13-secbutyl-5-O-dedesosminyl-5-O-mycaminosyl erythromycin A and B

Cultures of *S. erythraea* JC2ΔeryCIIIpLS025 are extracted using methods described in the General Methods section and the crude extracts are dissolved in 5 ml of methanol and subsequently fed to culture supernatants of the *S. erythraea* strain SGQ2pSG144*8/27/95/21/44/193/6eryCIII* using standard techniques. The bioconversion of 13-desethyl-13-methyl-3-*O*-mycarosyl erythronolide B, 13-desethyl-13-isopropyl-3-*O*-mycarosyl erythronolide B and 13-desethyl-13-secbutyl-3-*O*-mycarosyl erythronolide B to 13-desethyl-13-methyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A and 13-desethyl-13-methyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin B; 13-desethyl-13-isopropyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A and 13-desethyl-13-isopropyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin B;13-desethyl-13-secbutyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A and 13-desethyl-13-secbutyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin B is verified by LCMS analysis.

Example 9: 13-desethyl-13-methyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A and 13-desethyl-13-methyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin B

Production of 13-desethyl-13-methyl-3-O-mycarosyl erythronolide B

Plasmid pIB023 (Patent application no 0125043.0), a pCJR24-based plasmid containing the DEBS1, DEBS2 and DEBS3, was used to transform *S. erythraea* JC2ΔeryCIII using standard techniques. The transformant JC2ΔeryCIIIpIB023 was isolated and cultures were grown using standard protocols, extracted and the crude extract was assayed using methods described in the General Methods section. The production of 3-*O*-mycarosyl erythronolide B, and 13-desethyl-13-methyl-3-*O*-mycarosyl erythronolide B is verified by LCMS analysis.

*Production of 13-desethyl-13-methyl-5-*O*-dedesosaminyl-5-O-mycaminosyl erythromycin A, 13-desethyl-13-methyl-5-*O*-dedesosaminyl-5-O-mycaminosyl erythromycin B*

Cultures of *S. erythraea* JC2ΔeryCIIIpIB023 are extracted using methods described in the General Methods section and the crude extracts are dissolved in 5 ml of methanol and subsequently fed to culture supernatants of *S. erythraea* SGQ2pSG144*8/27/95/21/44/193/6eryCIII* using standard techniques. The bioconversion of 13-desethyl-13-methyl-3-*O*-mycarosyl erythronolide B to 13-desethyl-13-methyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin A and 13-desethyl-13-methyl-5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin B are verified by LCMS analysis.

Example 10: Production of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin

Azithromycin aglycones were prepared using methods described in EP1024145A2 (Pfizer Products Inc. Groton, Connecticut). The *S. erythraea* strain SGT2pSG142 was isolated using techniques and plasmid constructs described earlier (Gaisser *et al.*, 2000). Feeding experiments are carried out using methods described previously (Gaisser *et al.*, 2000) with the *S. erythraea* mutant SGT2pSG142 thus converting azithromycin aglycone to 3-*O*-mycarosyl azithronolide. Biotransformation experiments are carried out using *S. erythraea* SGQ2pSG144*8/27/95/21/44/193/6eryCIII* and crude extracts containing 3-*O*-mycarosyl azithronolide are added using standard microbiological techniques. The bioconversion of 3-*O*-mycarosyl azithronolide to 5-*O*-dedesosaminyl-5-*O*-mycaminosyl azithromycin is verified by LCMS analysis.

Example 11: Production of 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin C

Isolation of the S. erythraea *mutant SGP1 (SGQ2ΔeryG)*

To create a chromosomal deletion in *eryG*, construct pSGΔG3 was isolated as follows: Fragment 1 was amplified using primers BIOSG53 5'-GGAATTCGGCCAGGACGCGTGGCTGGTCACCGGCT –3' (SEQ ID NO: 54) and BIOSG54 5'-GGTCTAGAAAGAGCGTGAGCAGGCTCTTCTACAGCCAGGTCA –3' (SEQ ID NO: 55) and genomic DNA of *S. erythraea* was used as template. Fragment 2 was amplified using primers BIOSG55 5'-GGCATGCAGGAAGGAGAGAACCACGATGACCACCGACG-3' (SEQ ID NO: 56) and BIOSG56 5'-GGTCTAGACACCAGCCGTATCCTTTCTCGGTTCCTCTTGTG-3' (SEQ ID NO: 57) and genomic DNA of *S. erythraea* was used as template. Both DNA fragments were cloned into *Sma*I cut pUC19 using standard techniques, plasmids pUCPCR1 and pUCPCR2 were isolated and the sequence of the amplified fragments was verified. Plasmid pUCPCR1 was digested using *Eco*RI/*Xba*I and the insert band DNA was isolated and cloned into *Eco*RI/*Xba*I digested pUC19. Plasmid pSGΔG1 is isolated using standard methods and digested with *Sph*I/*Xba*I followed by a ligation with the *Sph*I/*Xba*I digested insert fragment of pUCPCR2. Plasmid pSGΔG2 is isolated using standard procedures, digested with *Sph*I/*Hin*dIII and ligated with the *Sph*I/*Hin*dIII fragment of pCJR24 (Rowe *et al.*, 1998) containing the gene encoding for thiostrepton resistance. Plasmid pSGΔG3 is isolated and used to delete *eryG* in the genome of *S. erythraea* strain SGQ2 using methods described previously (Gaisser *et al.*, 1997; Gaisser *et al.*, 1998) and the *S. erythraea* mutant SGP1 (SGQ2ΔeryG) is created.

Production of 5-O-dedesosaminyl-5-O-mycaminosyl erythromycin C

The *S. erythraea* strain SGP1 (*S. erythraea* SGQ2ΔeryG) is isolated using standard techniques and consequently used to transform the cassette construct pSG144*8/27/95/21/44/193/6eryCIII* as formerly described. The *S. erythraea* strain SGP1pSG144*8/27/95/21/44/193/6eryCIII* is isolated and used for biotransformation as described in Example 2 and assays are carried out as described above to verify the conversion of 3-*O*-mycarosyl-erythronolide B to 5-*O*-dedesosaminyl-5-*O*-mycaminosyl erythromycin C by LCMS analysis.

Example 12: Production of 3-*O*-angolosaminyl-erythronolide B

Bioconversion of erythronolide B with S. erythraea Q42/1 pSG1448/27/91/4spnOp5/24/193/6angMII (pSG144angAIangAIIangMIIIspnOpangorf14angBangMIangMII)

Biotransformation experiments feeding erythronolide B were carried out as described in General Methods and the cultures were analysed. Angolosaminylated erythronolide B was detected. About 30 mg of 3-*O*-angolosaminyl-erythronolide B were isolated and the structure was confirmed by NMR analysis.

Table IV: ^{1}H and ^{13}C NMR for the 3-angolosaminyl-erythronolide B in $CDCl_3$

Position		δ_C	δ_H (mult., Hz)	H-H COSY	H-C HMBC
1	COO	176.3	-	-	-
2	CH	44.5	2.81 dq(10.4, 6.7)	3, 16	1,
3	CH	89.7	3.66 dd (10.5, 10.5)	2,	1, 2, 4, 5, 16, 17, 1'
4	CH	36.5	1.99 m	17	5, 6, 17
5	CH	81.5	3.69 bs		3, 6, 7, 17, 18
6	C	75.2	-		-
7	CH_2	38.3	1.92 dd (14.6, 9.0)	7b, 8	6, 8, 9, 18, 19
			1.44 dd (14.6. 5.4)	7a, 8	6, 8, 9, 18
8	CH	43.4	2.69m	7	7, 9, 18
9	CO	217.8	-		-
10	CH	40.1	2.91 bq (6.6)	20	9, 11, 20
11	CH	70.6	3.78 d (10.0)	12	12, 13, 20
12	CH	40.2	1.69 m	11, 21	13, 21
13	CH	75.6	5.40 dd (9.5, 9.3)	14	1, 11, 12, 14, 15, 21
14	CH_2	25.8	1.71 qd (7.2, 2.2)	13, 14b, 15	12, 13
			1.51 m	13, 14a, 15	13
15	CH_3	9.1	0.90 d (7.7)	14	
16	CH_3	15.2	1.19 d (6.9)	2	2, 3
17	CH_3	8.3	1.06 d (6.7)	4	3, 4, 5
18	CH_3	26.6	1.30 s		5, 6, 7
19	CH_3	16.9	1.16d (6.1)		1
20	CH_3	8.5	0.98 t (7.7)	10	9, 10, 11
21	CH_3	10.4	0.89 d (7.7)	12	11, 12, 13
1'	CH	103.0	4.61 dd (9.2, 1.6)	2'	2', 3', 3
2'	CH_2	27.0	1.49m	1', 2b, 3'	1', 3'
			2.00m	2a, 3'	1', 3', 4'
3'	CH	65.2	2.48 td (10.2, 3.5)	2', 4'	4'
4'	CH	70.3	3.03 dd (9.5, 9.5)	3', 5'	3', 5', 6'
5'	CH	73.9	3.34 dq (8.7, 6.0)	4', 6'	3'
6'	CH_3	17.5	1.34 d (6.0)	5'	4', 5'

Bioconversion of erythronolide B with S. erythraea 18A1 pSG1448/27/96/4p5/21/44/193/6angMII (pSG144angAIangAIIangorf4pangorf14angMIIIangBangMIangMII)

Biotransformation experiments feeding erythronolide B were carried out as described in General Methods and the cultures are analysed. Peaks characteristic for angolosaminylated erythronolide B were detected.

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